

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on:	August 20, 2006, 04:52:13 ; Search time (without a
	8895.537 M

**title:** US-10-643-829-1

**Perfect score:** 1431

**Sequence:** 1 ccgtccagaacgttcagcg.....ccggta

**Scoring table:** IDENTITY\_NUC

**Searched:** Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

**Minimum DB seq length:** 0

**Maximum DB seq length:** 200000000

**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

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Issued Patents_NA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7
6: /EMC_Celerra_SIDS3/ptodata/2/ina/8
7: /EMC_Celerra_SIDS3/ptodata/2/ina/9
8: /EMC_Celerra_SIDS3/ptodata/2/ina/9
9: /EMC_Celerra_SIDS3/ptodata/2/ina/9
10: /EMC_Celerra_SIDS3/ptodata/2/ina/

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Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score distribution

### SUMMARIES

#	Result No.	Score	Query Match Length	DB ID
1	1431	100.0	44378	3 US-09-949-016-12540
2	909.4	63.5	1237	3 US-09-007-678B-48
3	703.6	49.2	84875	3 US-09-949-016-17334
4	703.6	49.2	84875	3 US-09-949-016-17335
5	703.6	49.2	84875	3 US-09-949-016-17336
6	703.6	49.2	84875	3 US-09-949-016-17337
7	703.6	49.2	85152	3 US-09-949-016-12665
8	703.6	49.2	85152	3 US-09-949-016-12666
9	703.6	49.2	85152	3 US-09-949-016-12667
10	703.6	49.2	85152	3 US-09-949-016-12668
11	701	49.0	3798	3 US-09-023-655-887
12	281.2	19.7	512	3 US-09-949-016-4540
13	279.6	19.5	512	4 US-09-880-107-2282
14	279.4	19.5	9153	3 US-09-949-016-15183
15	249.2	17.4	187595	3 US-09-949-016-15546
16	247.8	17.3	422	3 US-09-397-787-186
17	220.6	15.4	3227	3 US-09-976-594-775
18	203.4	14.2	237	3 US-09-397-787-89
19	189.4	13.2	211049	3 US-09-949-016-15770
20	180.6	12.6	309	3 US-09-313-294A-7018
21	177	12.4	6727	3 US-09-949-016-16282
22	163.4	11.4	464	3 US-09-774-528-63
23	163.4	11.4	464	3 US-10-120-988-63

Total number of hits satisfying chosen parameters: 2807332  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Run on: August 20, 2006, 04:52:13 ; Search time 301 Seconds  
(without alignments)  
8895.537 Million cell updates/sec

## ALIGNMENT

Patent No. 5428012  
Patent No. 5451506  
Sequence 14089, A  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 17349, A  
Sequence 3441, Ap  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 14, Appl

Db 784 GGTCACTCATAGTCTCGAAGATGGGAGAGTAGATGCAGGAACGGAGACGGGA 843  
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 Db 844 GGCATAGGGGGAGGTGTGGGGCTGGGCTGCCGAGCGGGTACTCACGGATG 903  
 Qy 301 AAGTGAGGGTCTACCCCAACGGGGCTAGCTCTCGGAAGGACCGAACCTGGCG 360  
 Db 904 AAGTGAGGGTCTACCCCAACGGGGCTAGCTCTCGGAAGGACCGAACCTGGCG 963  
 Qy 361 GCAGCCGAGGAAGGGTTCCACAGTTAATTATCTGAATTCCACGCTTACTGTT 420  
 Db 964 GCAGCCGAGGAAGGGTTCCACAGTTAATTATCTGAATTCCACGCTTACTGTT 1023  
 Qy 421 GCCACGGAAACCGCTGAGCAATAGCTCTCAGAATAGGAATCAAGACACAGTCAGAGGA 480  
 Db 1024 GGCACGGAAACCGCTGAGCAATAGCTCTCAGAATAGGAATCAAGACACAGTCAGAGGA 1083  
 Qy 481 AGGCAGGGACAGAAAGAGCTAGCATCTCGGGCTCTGGTTGGCCACCCAGTCCTCC 540  
 1084 AGGGGGGACAGAAAGAGCTAGCATCTCTCGGGCTCTGGTTGGCCACCCAGTCCTCC 1143  
 Qy 541 CCTGCTGACATAAAAGAAAGAGAGGAAAGGAATTCTACCTGAGTCGGCTAA 600  
 1144 CCTGCTGACATAAAAGAAAGAGAGGAAAGGAATTCTACCTGAGTCGGCTAA 1203  
 Qy 601 GCGCCCGCCCTCTCGCCTCTACGCTTCCAGTGGGCTTATTACGTCAAGTAATGCTG 660  
 1204 GCGCCCGCCCTCTCGCCTCTACGCTTCCAGTGGGCTTATTACGTCAAGTAATGCTG 1263  
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 Qy 721 GTCTTAAGAAGGGTCCATTACCCACTCTTCCAGCTTAATGGAGGCTCCAGTTAG 780  
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 Qy 781 GTAAATAAAGGATGGGGAGGAAAGAACTACTATTCCACATGATGC 840  
 Db 1384 GTAAATAAAGGATGGGGAGGAAAGAACTACTATTCCACATGATGC 1443  
 Qy 841 GGAACGAAAGGGCTGGCACACTGTCTGGAAACTGTGTTATGGAGGAAACAT 900  
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 Qy 1081 CCCACGGACTCTGGGCAAGTAGTCTTAAGGTCAGTGGCTCTGGGGACGGAGGGC 1140  
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 Qy 1141 GCGGAATTGCTGGGAAGGGAAATCCGCTCTGGCCACATCTGCCACTCTAGTC 1200  
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 Qy 1201 CGCCCTCAGCTCAATGTTGTTATGTTGTTAGGTCAAGGTGCTCTGCCCGCC 1260  
 Db 1804 CGCCCTCAGCTCAATGTTGTTATGTTGTTAGGTCAAGGTGCTCTGCCCGCC 1863  
 Qy 1261 CATGACGCCAATCTCACCATAATGGCGTGGTGGCGTCAAGGTGAGGAGC 1320

Db 1864 CATCGAGGAATCTCCACCAATCAATGGGTTGGTCTGGGACAAGGGTGTGAGGC 1923  
 Qy 1321 CAATCATCTGGGAAACACTCGGAGAACAGGGACTAGTACTGTTATCCGCCATG 1380  
 Db 1924 CAATCATCTGGGAAACACTCGGAGAACAGGGACTAGTACTGTTATCCGCCATG 1983  
 Qy 1381 TTAGATTCACCCACAGGGATAGGGCAGAGCCGGTAGGGACGGTCTTG 1431  
 Db 1984 TTAGATTCACCCACAGGGATAGGGCAGAGCCGGTAGGGACGGTCTTG 2034  
 ; RESULT 2  
 ; US-09-007-678B-48  
 ; Sequence 48, Application US/09007678B  
 ; Patent No. 6342483  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HOLT, JEFFREY T.  
 ; APPLICANT: JENSEN, ROY A.  
 ; APPLICANT: PAGE, DAVID L.  
 ; APPLICANT: OBERMILLER, PATRICE S.  
 ; APPLICANT: ROBINSON-BENTON, CHERYL L.  
 ; APPLICANT: THOMPSON, MARILYN E.  
 ; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER  
 ; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2  
 ; CURRENT APPLICATION NUMBER: US/09/007,678B  
 ; CURRENT FILING DATE: 1998-01-15  
 ; PRIOR APPLICATION NUMBER: 08/373,799  
 ; PRIOR FILING DATE: 1995-01-17  
 ; PRIOR APPLICATION NUMBER: 08/182,961  
 ; PRIOR FILING DATE: 1994-01-14  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: Microsoft WordPad  
 ; SEQ ID NO: 48  
 ; LENGTH: 1237  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-007-678B-48  
 Query Match 63.5%; Score 909.4; DB 3; Length 1237;  
 Best Local Similarity 94.0%; Pred. No. 6.6e-277;  
 Matches 999; Conservative 0; Mismatches 36; Indels 28; Gaps 4;  
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 Qy 381 CACAGTTAATTATCTGTAATCCCACGCTTACTGTTGCCACGGAA----- 429  
 Db 131 CGCAGTTAATTATCTGTAATCCCGCGCTTTCGCGTGCACCGAACCGGACT 190  
 Qy 430 ACCGCTGACCAATGCCTCTCGAATAGGAATCAAGACACAGTCAGAGGAGGGAG 489  
 Db 191 ACCGCTGACGACGCCTCTCGAATAGGAATCAAGGTACATCAGGGAGGGAG 250  
 Qy 490 CAGAAAGGCCATGACATCTCGGGCTCTGGGTTGGCCACCCAGTCTCCCTGG-TGA 548  
 Db 251 CAGAAAGGCCAAGGCTCTCGGGCTCTGGGTTGGCCACCCAGTCTGCCCGGATGA 310  
 Qy 549 CATAAAAAGAGAGACGGAAAGGAAGAATTCTACCTGAGTGGCGTAAGGGCCG 608  
 Db 311 CGTAAAGGAAAGGAGACGGAAAGGAATTCTACCTGAGTGGCGTAAGGGCCG 370  
 Qy 609 CCTCTCGCCTCTACGCTTCCAGTGGGGTTATTACGTACAGTAATGCTGTACCAAG 668  
 Db 371 CCTCTCGCCTCTACGCTTCCAGTGGGGTTATTACGTACAGTAATGCTGTACCAAG 430  
 Qy 669 TCAGAATCGCCACCTGAGGGCTGAATATCGCGTAAGTAGTGTGCTCAAAGCGTCTTAAG 728  
 Qy 431 TCAGAATCGCCACCTGAGGGCTGAATATCGCGTAAGTAGTGTGCTCAAAGCGTCTTAAG 490  
 Qy 729 AAGAGGTCCTACCCACTCTCCGCTTAATGGAGTGTGCTCAAAGCGTCTTAAG 788  
 Db 491 AAGAGTCCCATACCCACTCTCCGCTTAATGGAGTGTGCTCAAAGCGTCTTAAG 550  
 Qy 789 AAGGATGTGGGGAGGGAAAGAACTACTATTCCACATGCGTGGGAGGAA 848  
 Db 551 AAGGATGTGGGGAGGGAAAGAACTACTATTCCACATGCGTGGGAGGAA 610

QY 849 AGGCCTTGGCCACACTGTCTGGAAACTGTACTTATGGAGAGAACATCCAATCC 908  
Db 611 AGGCCTTGGCCACACTGTCTGGAAACTGTACTTATGGAGAGAACATCCAATCC 670  
QY 909 AAGCGGGCACAACTCTCACCGAATCCAGTGGATAGATTGGAGACCTCCGGGCTTAT 968  
Db 671 AAGGGGCACAACTCTCACCGAATCCAGTGGATAGATTGGAGACCTCCGGGCTTAT 730  
QY 969 ACATGTCAACAGTAATGGATTGGAGTGTGTATGGAGACCTCCGGGCTTAT 1028  
Db 731 ACATGTCAACAGTAATGGATTGGAGTGTGTATGGAGACCTCCGGGCTTAT 785  
QY 1029 AGGCCAAANAAAAGATAACCTACAACCTCTAGGAAGACTACGATCCCACCGA 1088  
Db 786 AGGCCAAANAAAAGATAACCTACAACCTCTAGGAAGACTACGATCCCACCGA 834  
QY 1089 GTCTCGGCAAGTAGTCCTAAGGTCACTGGCCTGCGGGCTGCGGGCTAAGGCCACCGA 1148  
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QY 1149 TGCCTGGGAAGGGAAATCCGCTCTGGCCACATCTGCGCACTCTAGTCCGCCCTC 1208  
Db 895 TGCTGGGAAGGGAAATCCCTCTCTGGTCACATCTGCGCACTCTAGTCCGCCCTC 954  
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Db 955 AGCCTCAATGTGTATGGTGTCTGGGTCAAGTGCTCTGCCGCCATCGACG 1014  
QY 1269 CAATCTCCACCAATCAATGGGTGTCTGGGTCAAGTGCTCTGCCGCCATCGACG 1328  
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QY 1329 TTGGCGAACACTCGGAGAACAGGGGACTAGTTACTGTCTTATCCGCATGTTAGATC 1388  
Db 1075 TTGGCGAACACTCGGAGAACAGGGGACTAGTTACTGTCTTATCCGCATGTTAGATC 1134  
QY 1389 ACCCACACAGGATAGGGCAGAGGCCGTAGGGACGGTCTTG 1431  
Db 1135 ACCCACACAGGATAGGGCAGAGGCCGTAGGGACGGTCTTG 1177

RESULT 3

US-09-949-016-17334/C  
; Sequence 17334, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; LENGTH: 84875  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-17334

Query Match 49.2%; Score 703.6; DB 3; Length 84875;  
Best Local Similarity 85.0%; Pred. No. 1e-210; 109; Indels 51; Gaps 9;  
Matches 910; Conservative 0; Mismatches 109; Insertions 51; Gaps 9;

QY 381 CACAGTTTAATTATCTGTAATCCACGGCTTACTGTGTGCCACGGAA-----429

Db 1732 CGCAGTTTAATTATCTGTAATCCCGCTTTCCGTCACGGAAAGGGCCT 1673  
QY 430 ACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACGTCAAGGAAGGGGGA 489  
Db 1672 ACCGCTAAGCAGGCCTCTCAGAATAGGAATCAAGTACAATCAGAGGATGGGGGA 1613  
QY 490 CAGAAGAGCTAGCATCTCTGGGGCTCTGGTTGGCCACCCAGTCCTCCCTGG-TGA 548  
Db 1612 CAGAAGAGCCAGGCTCTGGGCTCTGGATTGGAGACCTCCGGGGCTT 1553  
QY 549 CATAAAAAGAAAGAGACGGAAAGGAATCTACCTGAGTTCGGCTAAGGCCCGC 608  
Db 1552 CGTAAGAGGAAGAGACGGAGAGGAATTCTACCTGAGTTGCTGCCTAAGTGCTGC 1493  
QY 609 CCTCTCGCCTCTAGCTTCAGTTGCGGCTTATGCATCACAGTAATTGCTGTACGAAGG 668  
Db 1492 CCTCTAGCTCTACTCTCCAGTGTGCGGCTTATGCATCACAGTAATTGCTGTACGAAGG 1433  
QY 669 TCAGAATGCCACCTGTGAGGCTCTGAATATCAGGTAAGATAGTGTCAAAGCAGTCTTAAG 728  
Db 1432 TCAGAATCGCTAC-----TATGTTCCAAAGCAGTCGTAG 1397  
QY 729 AAGAGGTTCCATTACCCACTCTTCCGCTTAATGGAGGTCTCCAGTTAGGTAATAA 788  
Db 1396 AAGAGGTTCCAATCCCCACTCTTCCGCCCTAATGGAGGTCTCCAGTTAGGTAATA 1337  
QY 789 AAGGATTTGGGGAGG-G---AACTACTATTCCAACATGCATGGGA 843  
Db 1336 AAGTAAATAAGGATTTGGGGGGGGGGAAATAATTTCAGCATGGGTGGGA 1277  
QY 844 ACGAAAGGCCTGGCCACACTGTCTTGGAAACTGTAGTCCTATGGAGGAACATCCA 903  
Db 1276 ATGAAAGGTCTGCCACAGTTCTTCTAGAAACTGTAGTCCTATGGAGGAACATCCA 1217  
QY 904 ATACCAAAGGGGACAACTCTACGGGAATCCAGTGGATAGATGGAGAACCTCCGGGG 963  
Db 1216 ATACGAGGGGACAACTCTACGGGAATCCAGTGGATAGATGGAGAACCTGGGG 1157  
QY 964 CTTATACATGTCAACAGTAATGGATTGGAGTGTGTATGTTCTCTATTTGAGAGCAG 1023  
Db 1156 CTGTAATGTCAACAGTTATGGACTGGAG---TGTATGTTCTGTATTGAGAACAG 1100  
QY 1024 AGACTAGGCCAAAAAGATACCTACAAC-CTAGGAAGACTACGATCCCATCGCC 1082  
Db 1099 AAACTAGGCTTAAGAGATACTCTTAGGGAGACTACAATCCCATCGCC 1040  
QY 1083 CCACGGCTCTGGCAAGTAGTCTCTAAGGTCACTGGCCTGGGACGCCAGTGGGCC 1142  
Db 1039 CCACGGCTCTGGCAAGTAGTCTCTAAGGTCACTCTAGGGAGACTACAATCCCATCGCC 980  
QY 1143 CGAATTGCTGGGAAGGGAAATCCCTCTGGCCACATCTGGCACTCTAGTCC 1202  
Db 979 CGAATTGCTGGCAAGGGAAATGCGCTCTGGCCATGTGGCACTCGTAGTTCCA 920  
QY 1203 CCCCTCAGCTCAATGTGTATGGTGTCTGGGTCAAGTTGCTCTGGGGGG-CCCC 1261  
Db 919 CCCCTCAGGCCCACTGTGTATGGTGTCTGGGTCAAGTTGCTCTGGGGGGCTTCTCC 863  
QY 1262 ATCGACGCAATCTCCACCAATCAATGGGGTGTCTGGGGGGCAAGTGGTGAAGGCC 1321  
Db 862 GTCGACGCCATGCCACCGTCAATGGGGTGTCTGGGGCAAGTGGTGAAGGCC 803  
QY 1322 AATCATCTTGGCGAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTATCCGCCATGT 1381  
Db 802 AATCTTCTGGCGAACCGGGGAAAC-GGGACTAGTTACTGTCTTATCCGCCATGT 745  
QY 1382 TAGATTCAACCCACAGGAGATGGCGAGAGGCCGGTAGGGACGGCTCTG 1431  
Db 744 TAGATTCAACCCACAGGAGATGGCGAGAGGCCGGTAGGGACGGCTCTG 695  
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US-09-949-016-17335/C

; Sequence 17335, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17335  
; LENGTH: 84875  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-17335

Query Match 49.2%; Score 703.6; DB 3; Length 84875;  
Best Local Similarity 85.0%; Pred. No. 1e-210;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;  
QY 381 CACAGTTAATTATCTGTAATTCCACGCTTACTGTGCCACGGAA----- 429  
Db 1732 CGCAGTTTAATTATCTGTAATTCCCGCGTTTCGGTGCACGGAAAGGGCT 1673  
QY 430 ACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACAGTCAGAGGAAGGGGAA 489  
Db 1672 ACCGCTTAAGCAGCCTCTCAGAATACGAATCAGGATGGAGATGGAGGA 1613  
QY 490 CAGAAAGAGCCTAGCATCTCGGGCTCTGGITGGCACCCAGTCCTCCCTGG-TGA 548  
Db 1612 CAGAAAGAGCCAAGGGTCTCTCGGGGCTCTGGCACCCAGTCCTGGGATGA 1553  
QY 549 CATAAAAGAAGAGACGGAAAGGAATTCTACCTGAGTCGGGTAAGGCCCGC 608  
Db 1552 CGTAAAGGAAGAGACGGAAAGGAGAATTCTACCTGAGTCGGCTAACAGTGGCTGC 1493  
QY 609 CCTCTCGCCTCTACGCTTCCAGTGCGCTTATAGTCACAGTACGGTACCAAGG 668  
Db 1492 CCTCTAGCCTACTCTCCAGTGCGCTTATGCATCACAGTAATTGCTGAGGA 1433  
QY 669 TCAGAATGCCACCTGAGCTGAATATCAGCTAACAGCAGTCCTTAAG 728  
Db 1432 TCGAAATCGCTACC-----TATTGTCACAGCAAGCAGTCGTAAG 1397  
QY 729 AAGGGTCCCTACCCACTTTGCCCTATGGAGGTCTCCAGTTAGGAAATAA 788  
Db 1396 AAGGGTCCCAATCCCCACTCTCCGCCCTATGGAGGTCTCCAGTTGGTAATAAT 1337  
QY 789 AAGGATTGTTGGAGGTGGAGGA-----ACTACTTCCAACATGCATGGGA 843  
Db 1336 AAGTATAAGGATTGTTGGGGGGTGGAGGAATAATTATCCAGATGCGTGGGA 1277  
QY 844 ACGAAGGCCTGGCCACACTGTTCTTGGAAACTGTAACCTTATGGAGGAACATCCA 903  
Db 1276 ATGAAAGGTCTGCCAACAGTGTCTTAGAAACTGTAACCTTATGGAGGAACATCCA 1217  
QY 904 ATACCAAAGGGCACATTCTACGGAAATCCAGTGGATAGATGGAGCCTCCGGGG 963  
Db 1216 ATACCAAGGGCACATTCTACGGAAATCCAGTGGATAGATGGAGCCTGGCG 1157  
QY 964 CTTATACATGTCACAGTATGGATTGGAGTGTGTATGTTCTCTATCTGAGAGCAG 1023  
Db 1156 CTTGTACTGTCAACAGTATGGACTGGAG-----TGTATGTTGAAAGCAG 1100  
QY 1024 AGACTAGGCCAAAAAGATACTTACCACTC-CTAGGAAGACTACGATCCCATCCAGCC 1082

Db 1099 AACTAGGCCTTAAAGATACTGTACAATCTTAGGGAGACTACAATTCCCATCCAGCC 1040  
QY 1083 CCACGAGTCTCGGGCAAGTAGTCCTCTAAGTCAGTGGCTCGGGAGCGACTGGGGCG 1142  
Db 1039 CCAGGACTCTGGCAAGTAGTCCTCTAAGTCAGTGGCTCGGGAGCGACTGGGGCG 980  
QY 1143 CGAATRTGCTGGGAAGGGAAATCCGCTCTGGCCACATCTGCGACTCCTAGTTCCG 1202  
Db 979 CGAATRTGCTGGGAAGGGAAATGCCCTCTGGCCATGTCTGCGCACTCGTAGTCCA 920  
QY 1203 CCCCTAGCCTCAATGTTGTTATGTTGTTGGGTCAGGTGCTTCGCCCCG-CCCC 1261  
Db 919 CCCCTAGCCCCAGTGTGTTA---TTRTCGGGTCAGCTGCTTCCCCTGTC 863  
QY 1262 ATCGACGCAATCTCCACCAATCAATGGGTTGGTGTGTTGAGGACAAGTGGTGAAGGCC 1321  
Db 862 GTGGACGCAATGCCACCCAGTCATGGGTTGGTGTGTTGAGGACAAGTGGTGAAGGCC 803  
QY 1322 AATCATCTGGGAAACACTGGAGAACAGGGACTAGTTACTGTCTTATGCCATG 1381  
Db 802 AATCTCTGGGAAACGGGAGACGCTGGCACGGACGGTCTCCGCCATG 745  
QY 1382 TAGATTCCCCACAGGGATAGGGCAGAGCCGGTAGGGACGGTCTTG 1431  
Db 744 TAGATTCCCCACAGAGATAGGGCACGGAGCTGGCACGGTCTTG 695

RESULT 5  
US-09-949-016-17336/c  
; Sequence 17336, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17336  
; LENGTH: 84875  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-17336

Query Match 49.2%; Score 703.6; DB 3; Length 84875;  
Best Local Similarity 85.0%; Pred. No. 1e-210;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;  
QY 381 CACAGTTAATTATCTGTAATTCCACGCTTACTGTGCCACGGAA----- 429  
Db 1732 CGCAGTTTAATTATCTGTAATTCCCGCGTTTCGGTGCACGGAAAGGGCT 1673  
QY 430 ACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACAGTCAGAGGAAGGGGAA 489  
Db 1672 ACCGCTTAAGCAGCCTCTCAGAATACGAATCAGGATGGAGATGGAGGA 1613  
QY 490 CAGAAAGAGCCTAGCATCTCGGGCTCTGGITGGCACCCAGTCCTCCCTGG-TGA 548  
Db 1612 CAGAAAGAGCCAAGGGTCTCTCGGGGCTCTGGCACCCAGTCCTGGGATGA 1553  
QY 549 CATAAAAGAAGAGACGGAAAGGAATTCTACCTGAGTCGGGTAAGGCCCGC 608  
Db 1552 CGTAAAGGAAGAGACGGAAAGGAGAATTCTACCTGAGTCGGCTAACAGTGGCTGC 1493



**RESULT 7**  
**US-09-949-016-12665/c**  
; Sequence 12665, Application US/09949016  
; Patent No. 6812339

**GENERAL INFORMATION:**

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 12665  
LENGTH: 85152  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12665

**Query Match**  
Best Local Similarity 85.0%; Pred. No. 1e-210; Length 85152;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

**Qy** 381 CACAGTTAATTATCTGTAATTCCACGGTTACTGTGCCACGGAA----- 429  
Db 2009 CGCAGTTTAATTATCTGTAATTCCCGCGTTTCGGTGCACGGAAAGGGCT 1950

**Qy** 430 ACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACAGTCAGGAAGGGGG 489  
Db 1949 ACCGCTAAGCAGCAGCCTCTCAGAACATCAAGGTACAATCAGGATGGGG 1890

**Qy** 490 CAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGTGGCCACCCAGTCCCCTGG-TGA 548  
Db 1889 CAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGTGGCCACCCAGTCCCCTGG-TGA 1830

**Qy** 549 CATAAAAGAAGAGACGGAAAGGAGATTCTACCTGAGTCGCCGTAAGGCCCGC 608  
Db 1829 CCTTAAGGAAGAGACGGAAAGGAGATTCTACCTGAGTCGCCGTAAGGCCCGC 1770

**Qy** 609 CCTCTCGCCTCTACGCTTCAAGTGAGTCGCCGTAAGGCCCGC 668  
Db 1769 CCTCTAGCTCTACTCTCCAGITGCCGTTATGCATCACGTAATTGTGAGG 1710

**Qy** 669 TCAGAATGCCACCTGAGCTGAATATCAGCTAACAGGACTTAAG 728  
Db 1709 TCAGAATCGCTACC-----TATGTCCAAGCAGTCGAAG 1674

**Qy** 729 AAGGGTCCATTACCCACTTCCGCTTAATGGAGTCTCAGTTAGTAATAA 788  
Db 1673 AAGGGTCCAACTCCCCACTCTTCCGCCTATGGAGTCCTCCAGTTCCGTAAT 1614

**Qy** 789 AAGGATGTTGGAGGTGGAGGAAG-----ACTACTATTCACATGCTGGGA 843  
Db 1613 AAGTATAAGGATGTTGGGGGGTGGAGGAATAATTTCAGCATGCTGGGA 1554

**Qy** 844 ACGAAAGGCCCTGGCCACACTGTCCTTGGAAACTGTAGTCATTGGAGAGAACATCCA 903  
Db 1553 ATGAAGGTCTCGCCACAGTGTCTTAGAAACTGTAGTCATTGGAGAGAACATCCA 1494

**Qy** 904 ATACCAAAGCGGCCACAATTCTCACGGAATCCAGTGGATAGATTGGAGACCTCCGGGG 963  
Db 1493 ATACCAAAGCGGCCACAATTCTCACGGAATCCAGTGGATAGATTGGAGACCTCCGGGG 1434

**Qy** 964 CTTATACATGTCACAGTAATTGGATTGGAGTGTCTTATGTGAGAGCAG 1023  
Db 1433 CTGTACTTGTCAACAGTTAGGACTGGAG---TGTATGTTTCGTATTGAAAGCAG 1377

**Qy** 1024 AGACTAGGCCAAMAAGATACTACACT-CTAGGAAGACTACGATCCCACATCCGCC 1082  
Db 1316 AAACTAGGCCTAAAGATACTGTCACACTCTTGTGGAGACTACATCCCATCCGCC 1317

**Qy** 1083 CCACGAGTCTCGGCAAGTAGTCTCTAGGTCACTGGCTCGGGGACCGCAGTGGCGC 1142  
Db 1256 CGAATTGCGCTGGGCAAGTAGTCAGTCACTCTTGTGGAGACTACATCCGCC 1257

**Qy** 1143 CGAATTGCGCTCAATGTTGTTATGTGTCGGGTCAGGTGCTCTGCCCCG-CCCC 1202  
Db 1196 CCCCTCAGCCCCAGTGTGTTA---TTRTCGGGTCAGCTGCTTTCGCCCCGTCTCC 1140

**Qy** 1262 ATCGACGCAATCTCCACCAATCAATGGGTGTCGTTTGAGGACAAGGGTGAAGGCC 1321  
Db 1139 GTCGACGCAATGCCACCACTCAATGGGTGTCGTTTGAGGACAAGGGTGAAGGCC 1080

**Qy** 1322 AATCATCTTGGGAAACTGGGAGAACAGGGACTAGTTACTGTCTTATCGCCATGT 1381  
Db 1079 AATCTCTTGGGAAACGGGAGAAC-GGGACTAGTTACTGTCTTGTCCGCCATGT 1022

**Qy** 1382 TAGATTCAACCCACAGGAGATAGGGCAGAGCCGTTAGGGACGGCTCTTG 1431  
Db 1021 TAGATTCAACCCACAGGAGATAGGGCAGAGCTGGCAGGGCTTTCG 972

**RESULT 8**  
**US-09-949-016-12666/c**  
; Sequence 12666, Application US/09949016  
; Patent No. 6812339

**GENERAL INFORMATION:**

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-09-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 12666  
LENGTH: 85152  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12666

**Query Match**  
Best Local Similarity 85.0%; Pred. No. 1e-210; Length 85152;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

**Qy** 381 CACAGTTAATTATCTGTAATTCCACGGTTACTGTGCCACGGAA----- 429  
Db 2009 CGCAGTTTAATTATCTGTAATTCCCGCGTTTCGGTGCACGGAAAGGGCT 1950

QY 430 ACCGGCTGAGCAAATAGCCTCTCGAAATAGGAATTCAAGACACAGTCAGGGAGGGGG 489  
 Db 1949 ACGCTAAGCAGCAGCCCTCTCAGAAATCAAGGTACAATCAGGGATGGAGGA 1890  
 QY 490 CAGAAAGAGCTAGCATCTCGGGCTCTGGTGGCACCCAGCTCTCCCCTGG-TGA 548  
 Db 1889 CAGAAAGAGCCAAAGGCCTCTCGGGCTCTGGATGGCACCCAGCTGCC 1830  
 QY 549 CATAAAAGAAGAGACGGAAAGGAGAATTCTACCTGAGTTCGGTAAGGCGC 608  
 Db 1829 CGTAAAGGAAAGAGACGGAAAGGAGAATTCTACCTGAGTTCGGTAAGGCGC 1770  
 QY 609 CCTCTCGCCTCTACGCTCCAGTGGGGCTATTACGTCACAGTAATTGCTGTACCAAGG 668  
 Db 1769 CCTCTAGCCTACTCTCCAGTGGGGCTATTGCACTCACAGTAATTGCTGTACGAAGG 1710  
 QY 669 TCAGAAATGCCAACCTGAGGCCTGAATAATCAGCGTAAGATAGTGTCCAAGCAGCTTAAG 728  
 Db 1709 TCAAGAATCGCTAC-----TATTGTCACAGTAATTGCTGTACGAAG 1674  
 QY 729 AAGAGGTCCATTACCCACTTTCCGCCCTAATGGAGGTCCAGTTAGGTAATAA 788  
 Db 1673 AAGAGGTCCAAATCCCCACTTCCGCCCTAATGGAGGTCTCCAGTTGGTAATAA 1614  
 QY 789 AAGGATGTTGGAGGGTGGAGGAAG-----AACTACTATTCAAATGCAATTGGGA 843  
 Db 1613 AAGTAATAAGGATGTTGGGGGGTGGAGGAATAATTATTCCAGCATGCGTTGGGA 1554  
 QY 844 ACGGAAGGCCTGGCCACACTGTTCTTGAAACTGTAGTCTATGGAGAGGAATCCA 903  
 Db 1553 ATGAAAGGTCTCGCCACAGTGTCTTAGAAACTGTAGTCTTATGGAGAGGAACATCCA 1494  
 QY 904 ATACCAAAAGGGCACATTCTCAGGAATCCAGTGGATAATGGAGACCTCCGGGG 963  
 Db 1493 ATACCAAGGGCACATTCTCAGGAATCCAGTGGATAATGGAGACCTGTGGGG 1434  
 QY 964 CTTATACATGTCACAGTAATGGATGGAGTGTGTATGTTCTCATTCTGAGAGCAG 1023  
 Db 1433 CTGTACTTGTCAACAGTATGGAG-----TGTATGTTGTATTGAAAGCAG 1377  
 QY 1024 AGACTAGGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCATCCAGCC 1082  
 Db 1376 AACTAGGCCTTAAAGATACTACACTTCTAGGAGACTACGATCCATCCAGCC 1317  
 QY 1083 CCACGAGTCTGGCAAGTAGTCTCTAAGGTCACTACACTC-CTAGGAAGACTACGATCCAGCC 1142  
 Db 1316 CCACGAGTCTGGCAAGTAGTCTCTAAGGTCACTACACTC-CTAGGAAGACTACGATCCAGCC 1257  
 QY 1143 CGAAATTGCTCGGAAGGGAAATCCGCTCTGGCCACATCTGCCACTCTAGTTCC 1202  
 Db 1256 CGAAATTGCTCGGGCAAGGGAAATGCCCTCTGGCCACTCTGTAGTTCCA 1197  
 QY 1203 CCCCTCAGCCTCAATGTTGTTATGTTGTCAGGTGCTCTGCCCG-CCCC 1261  
 Db 1196 CCCCTCAGGCCAGGTGTTGTTA---TTTTTCTGGGTCAGCTGCC 1140  
 QY 1262 ATCGACGCAATCTCACCATACTGGGCGTTCTGGGCAAGTGGTGAAGGCC 1321  
 Db 1139 GTCCGACGCAATGCCACCGTCAATCGGGTGGTGTGGAGAACAGGCC 1080  
 QY 1322 AATCATCTGGGAGACACTCGGAGAACAGGGACTAGTACTGTTTATCCGCATGT 1381  
 Db 1079 AATCTTCTGGGAACAGGGAAAC-GGGACTAGTACTGCTTCCTCCGCATGT 1022  
 QY 1382 TAGATTCAACCCACAGGGATAGCGGAGAGCCGGTAGGGACGGTCTTG 1431  
 Db 1021 TAGATTCAACCCACAGAGATAGCGGGAGCTGGCAGCGGACGGTCTTG 972

; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIORITY NUMBER: 60/237,768  
; PRIORITY DATE: 2000-10-03  
; PRIORITY NUMBER: 60/231,498  
; PRIORITY FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SEQ ID NO 12667  
; LENGTH: 85152  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-12667

Query Match Score 703.6; DB 3; Length 85152;  
 Best Local Similarity 85.0%; Pred. No. 1e-210; Mismatches 109; Indels 51; Gaps 9;  
 Matches 910; Conservative 0;

QY	Db	Score	DB	Length
381	2009	49.2%	3	85152
CACAGTTTAATTATCTGTAATTCCACGCTTACTGTTGCAACGGAA-----	CGCAGTTTAATTATCTGTAATTCCACGCTTACTGTTGCAACGGAA-----	703.6	3	85152
430	430	49.2%	3	85152
ACCGCTGAGCAAATGCGCTCTCGAAATAGGAATTCAGACACAGTCAGGGAGGA 489	ACCGCTGAGCAAATGCGCTCTCGAAATAGGAATTCAGACACAGTCAGGGAGGA 489	703.6	3	85152
1949	1949	49.2%	3	85152
ACCGCTAAGCAGCAGCCCTCTCGAAATAGGAATTCAGACACAGTCAGGGAGGA 1890	ACCGCTAAGCAGCAGCCCTCTCGAAATAGGAATTCAGACACAGTCAGGGAGGA 1890	703.6	3	85152
490	549	49.2%	3	85152
CAGAAAGAGCTAGCATCTCTGGGGCTCTGGGTTGGCCACCCAGTCTCCCTGG-TGA 548	CAGAAAGAGCTAGCATCTCTGGGGCTCTGGGTTGGCCACCCAGTCTCCCTGG-TGA 548	703.6	3	85152
609	609	49.2%	3	85152
CCTCTCGCCTCTAGCTCCAGTTGTCAGGAGACTACGATCCATCCAGCC 1494	CCTCTCGCCTCTAGCTCCAGTTGTCAGGAGACTACGATCCATCCAGCC 1494	703.6	3	85152
668	1769	49.2%	3	85152
CCTCTAGCCTACTCTCCAGTTGGCTTGCCTTATGCACTCACAGTAATTGCTGTACGAAG 1710	CCTCTAGCCTACTCTCCAGTTGGCTTGCCTTATGCACTCACAGTAATTGCTGTACGAAG 1710	703.6	3	85152
728	1709	49.2%	3	85152
TGAGGATGGCTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	TGAGGATGGCTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	703.6	3	85152
843	1613	49.2%	3	85152
AAGTAATAAGGATGTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	AAGTAATAAGGATGTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	703.6	3	85152
903	1553	49.2%	3	85152
ACGAAAGGGCACATTCTCAGGGAAATCCAGTGGTGTCTGGGCA 1434	ACGAAAGGGCACATTCTCAGGGAAATCCAGTGGTGTCTGGGCA 1434	703.6	3	85152
963	1433	49.2%	3	85152
AGACTAGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCACGCC 1023	AGACTAGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCACGCC 1023	703.6	3	85152
1082	1433	49.2%	3	85152
CTGTACTTGTCAACAGTATGGAGTGTCTTGTATTGAAAGCAG 1377	CTGTACTTGTCAACAGTATGGAGTGTCTTGTATTGAAAGCAG 1377	703.6	3	85152
1317	1316	49.2%	3	85152
CCACGAGTCTGGCAAGTAGTCTCTAAGGTCACTACACTC-CTAGGAAGACTACGATCCAGCC 1257	CCACGAGTCTGGCAAGTAGTCTCTAAGGTCACTACACTC-CTAGGAAGACTACGATCCAGCC 1257	703.6	3	85152
1376	1376	49.2%	3	85152
AGACTAGGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCACGCC 1082	AGACTAGGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCACGCC 1082	703.6	3	85152
1434	1434	49.2%	3	85152
AGACTAGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCACGCC 1023	AGACTAGCCAAAAAGATACTACACTC-CTAGGAAGACTACGATCCACGCC 1023	703.6	3	85152
1494	1493	49.2%	3	85152
ATACCAAGGGCACATTCTCAGGGAAATCCAGGGATAGTGGAGACCTGGGCA 1434	ATACCAAGGGCACATTCTCAGGGAAATCCAGGGATAGTGGAGACCTGGGCA 1434	703.6	3	85152
1554	1553	49.2%	3	85152
ACGAAAGGGCACATTCTCAGGGAAATCCAGGGATAGTGGAGACCTGGGCA 1434	ACGAAAGGGCACATTCTCAGGGAAATCCAGGGATAGTGGAGACCTGGGCA 1434	703.6	3	85152
1614	1613	49.2%	3	85152
AAGTAATAAGGATGTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	AAGTAATAAGGATGTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	703.6	3	85152
1714	1709	49.2%	3	85152
TGAGGATGGCTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	TGAGGATGGCTTGGGGGGTGGAGGAATAATTGCGTGTAGTGTCCAAAGCAGCTTAA 788	703.6	3	85152
1770	1769	49.2%	3	85152
CCTCTAGCCTACTCTCCAGTTGGCTTGCCTTATGCACTCACAGTAATTGCTGTACGAAG 1710	CCTCTAGCCTACTCTCCAGTTGGCTTGCCTTATGCACTCACAGTAATTGCTGTACGAAG 1710	703.6	3	85152
1890	1889	49.2%	3	85152
AGAAAGGGCACATTCTCAGGGAAATCCAGGGATAGTGGAGACCTGGGCA 1830	AGAAAGGGCACATTCTCAGGGAAATCCAGGGATAGTGGAGACCTGGGCA 1830	703.6	3	85152
1949	1949	49.2%	3	85152
ACCGCTAAGCAGCAGCCCTCTCGAAATAGGAATTCAGACACAGTCAGGGAGGA 1890	ACCGCTAAGCAGCAGCCCTCTCGAAATAGGAATTCAGACACAGTCAGGGAGGA 1890	703.6	3	85152

RESULT 10  
US-09-949-016-12668/c

; Sequence 12668, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12668

LENGTH: 85152

TYPE: DNA

ORGANISM: Human

US-09-949-016-12668

Query Match 49.2%; Score 703.6; DB 3; Length 85152;  
Best Local Similarity 85.0%; Pred. No. 1e-210;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

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RESULT 11  
US-09-023-655-887/c

; Sequence 887, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

---

Db 1769 CCTCTAGCCTACTCTCCAGTTGCCCTATTGCATCACAGTAATTGCGTACGAAGG 1710

Qy 669 TCAGATGCCACCTGAGCCTGAATACTAGCGTAAGTAGTCTCAAGCAGTCTAAG 728

Db 1316 CCAGGAGTCGGGCAAGTAGTCCTGTAAGGTCACTGGCCCTGGGGACCGAGTGGCC 1257

Qy 1143 CGAATTGCGCTGGGAAGGGAAATTCCGCTCTGGCCACATCTGGCACTCTAGTCCG 1202

Db 1256 CGAATTGCGCTGGGCAGGGAAATCGCTCTGGCCATGTCGCGCACTCGTAGTCCA 1197

Qy 1203 CCCCTCAGCCTCAATGTTGTTATGTTGTTGGGTTCAGGTGCTTCAGTTAGGTAATTA 788

Db 1196 CCCCTCAGCCCCAGTGTGTTA---TTTTCGGGTTCACTGCTTGCCACTCGTAGTCCA 1140

Qy 1262 ATCGACGCAATCTCCACCAATCGGAGAACAGGGACTAGTTACTGTCCTTATCCGCATGT 1321

Db 1139 GTCGACGCAATCGGCCACCGAGTCATGGGGAGAACAGGGACAGTGGAGAGCC 1080

Qy 1079 ATCTCTTGGGAAACGGGAGAACAGGGACTAGTTACTGTCCTTGTCCCCGCTCC 1022

Db 1613 AAGAGTCCAATCCCCACTCTTCGCCCTAATGGAGGTCTCCAGTTCGGTAATAT 1614

Qy 789 AAGGATGTTGGAGGTGGAAAG----AACTACTATCCACATGCATGGGA 843

Db 844 ACAGAMGGCTGGCCACACTGTTCTGGGGAGAAATATTCCAGCATGGCTGGGA 1554

Db 1553 ATGAAGGTCTGGCACAGTGTGGTCTGGCTTGG 972

Qy 904 ATACCAAAGGGGACAATTCTACGGAATCCAGTGGATAGATGGAGAGGAACATCCA 903

Db 1493 ATACCAAAGGGGACAATTCTACGGAATCCAGTGGATAGATGGAGAGGAACATCCA 1494

Qy 964 CTTATACATGTCACAGTTATGGACTGGAG---TGTATGTTTTCGTTATTGGAAGCAG 1023

Db 1433 CTGTACTTGTCACTGTTGAGGAGCTGGGACAGTGTCTTGGAGACCTGGGG 1434

Qy 1024 AGACTAGGCCAAAAAGATACTACAACTC-CTAGGAAGACTACGATCCCATCCGCC 1082

Db 1376 AAATAGGCTTAAGATACTACAACTCCTTGGAGACTACAACTCCATCCGCC 1317

Qy 1083 CCACGACTCTGGCAAGTAGTACTCTTAAGTCAGTGGCCTGGGGACGCCAGTGGGCC 1142

Db 1316 CCCCTCAGCCCCAGTGTGTTA---TTTTCGGGTTCACTGCTTGCCCATGTCGAGGCC 1257

Qy 1143 CGAATTGCGCTGGGAAGGGAAATCCGCTCTGGCCACATCTGCACTCTAGTCCG 1202

Db 1256 CGAATTGCGCTGGGCAGGGAAATGCGCTCTGGCCCATGTCGCACTCGTAGTCCA 1197

Db 1203 CCCCTCAGCCTCAATGTTGTTATGTTGTTGGGTCAGGTTGCTCTGGGGGG-CCCC 1261

Db 1196 CCCCTCAGCCCCAGTGTGTTA---TTTTCGGGTTCACTGCTTGCCCATGTCG 1140

Qy 1262 ATCGACGCAATCTCCACCAATCGGAGTCGGCTGGTCTTGAAGGACAAGTGGTAGAGCC 1321

Db 1139 GTCGACGCAATCGGCCACCGACTCAATGGGTCTGGTCTTGGGAGAGCC 1080

Qy 1322 ATCGACGCAATCTCCACCAATCGGAGAACAGGGACTAGTTACTGTCCTTACGGCCATGT 1381

Db 1079 ATCTCTTGGGAAACGGGAGAACAGGGACTAGTTACTGTCCTTGGCCATGT 1022

Qy 1382 TAGATTCAACCCACAGGGATAGGGCAGAGGCCAGGGTAGGGACGGTCTTG 1431

Db 1021 TAGATTCAACCCACAGAGATAAGGGCAGAGGCCAGGGTCTTG 972

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/023,655  
 FILING DATE: HEREWITH  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 887:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3798 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: 91147602  
 ; US-09-023-655-887

Query Match 49.0%; Score 701; DB 3; Length 3798;  
 Best Local Similarity 84.9%; Pred. No. 1.1e-210; Mismatches 0; Indels 111; Gaps 51; Matches 908; Conservative 0; MisMatches 0; Indels 0; Gaps 9;

QY 381 CACAGTTAACATTCTGTAATCCACCGCTTACTGTTGCCACGGAA----- 429  
 Db 1589 CGCAGTTTAATTATCTGTAATCCGGCTTCGGTGCACGGAAAGGGCT 1530  
 QY 430 ACGCGCTGAGCAATAGCCTCTCGAATAGGAATAGACACAGTCAGAGGAAGGGGG 489  
 Db 1529 ACGGCTAACGGCAGCAGCCTCTCGAATAGGAATACGTAACTCAGAGGTGGGG 1470  
 QY 490 CAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGGTGGCCAACCGAGTCCCCTG-TGA 548  
 Db 1469 CAGAAAGAGCCAGCGTCTCGGGCTCTGGGACAGTCTGCCCGGATGA 1410  
 QY 549 CATAAAAGAAGAGAGCGAAAGGAGAATTCTACCTGAGTTGCCCTAAAGGCCCGC 608  
 Db 1409 CGTAAAGGAAGAGACGGAAAGGAGAATTCTACCTGAGTTGCCATAAGTGCCTGC 1350  
 QY 609 CCTCTCGCCTCTACGCTTCCAGTTCGGCTTATACGTCAAGTAATTGTCACAAGG 668  
 Db 1349 CCTCTAGCTCTACTCTTCCAGTTCGGCTTATGCACTCACGTAATTGCTGTACGAAGG 1290  
 QY 669 TCAGAATGCCAACCTGAGGCCTGAATATCAGCGTAAGATAGTGTCACAGCAAGGCTTAAG 728  
 Db 1289 TCAAGAATCGCTACC-----TATTGTCCAAAGCAGTGTCAAG 1254  
 QY 729 AAGGGTCCATTACCCACTCTCCCTATGGGGCTCCAGTTAGGTAATAA 788  
 Db 1253 AAGAGGTCCCAATCCCCACTCTTCCGCTATGGAGGTCTCAGTTGGTAATAT 1194  
 QY 789 AAGGATGTTGGGAGGTGGAGGAAG----ACTACTATTCCAAAGATGCATGGGA 843  
 Db 1193 AAGTAATAAGGATGTTGGGGGGTGGAGGAATAATTTCAGCATGGCTGGGA 1134  
 QY 844 ACGAAAGGCCTGGCCACACTGTTCCAGTGTAGCTTATGGAGGAACATCCA 903  
 Db 1133 ATGAAAGGTCTGCCACAGTGTCTTAGAAGTGTAGCTTATGGAGGAACATCCA 1074  
 QY 904 ATACCAAAGGGCACATTCTCACGGAATCCAGTGGATAGATTGGAGACCTCCGGGG 963  
 ; US-09-949-016-4540

RESULT 12  
 US-09-949-016-4540/C  
 ; Sequence 4540, Application US/09949016  
 ; Patent No. 6812339

GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 4540  
 LENGTH: 512  
 TYPE: DNA  
 ORGANISM: Human  
 ; US-09-949-016-4540

Query Match 19.7%; Score 281.2; DB 3; Length 512;  
 Best Local Similarity 91.4%; Pred. No. 2.5e-78; Mismatches 298; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 298; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Db 1073 ATACCAGAGGGGCCACAATTCTCACGGAATCCAGTGGATAGATTGGAGACCTGTGGCG 1014  
 QY 964 CTTATACATGTCAACAGTAATGGATTGGAGTGTATGTTCTCTATCTGAGACAG 1023  
 Db 1013 CTTGTAATGTCACAGTTATGGACTCGAG---TGTATGTTTCGTATTNGAAACAG 957  
 QY 1024 AGACTAGGCCAAMAAAGATACCTACACTC-CTAGGAAGACTACAGTCCATCCAGCC 1082  
 Db 956 AACTAGGCCTAAAGATACTACACTCTTAGGGAGACTACATTCATCCAGCC 897  
 QY 1083 CGACGAGCTCGGGCAAGTAGTCCTCTAAGGTCAAGTGGCTAGGGCTGGGGAGCGAGTGGCG 1142  
 Db 896 CCAGGAGCTGGGCCAAGTAGTGTCTGTAGGTCACTGGCCCTGGGGAGCGAGTGGCG 837  
 QY 1143 CGAATTGTGCTGGGAAGGGAAATCCGCTCTGGCCACATCTGCGACTCTAGTCCG 1202  
 Db 836 CGAATTGTGCTGGGCCAAGTAGTGTCTGTAGGTCACTGGCCCTGGGGAGCGAGTGGCG 777  
 QY 1203 CCCCTCAGCCTCAATGTTGTTATGTTGTTGGGTTCAGGTGCTCTGCCCCG-CCCC 1261  
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RESULT 13

US-09-880-107-2282/c

; Sequence 2282, Application US/09880107

; Patent No. 6974667

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; PRIOR FILING DATE: 2000-09-08

; SEQ ID NO 15183

; SOFTWARE: FastSEQ for Windows Version 4.0

; LENGTH: 9153

; TYPE: DNA

; ORGANISM: Human

; SEQ ID NO 15183

; LENGTH: 9153

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-15183

; Sequence 15183, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. CRAIG ET AL.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15183

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Best Local Similarity 90.6%; Pred. No. 4.9e-77;

Matches 298; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 2151 CCAGCCCTACATTCGAGATGAGGCTCCAAATGTTGACGTTGCCAGGCCTTGCAAC 2210

Query 110 AAGCCAGCCAAAAGTTCAATTACACTGGCTGCTTAATAAGGGCATTGATCTTA 169

Db 2211 AAGCCAGGCCAATAAGGTCACATTACACCGGCTGCTTATGAGGGCATTTGCAAC 2270

Query 170 TCCTCGTAAAGGTCACTCATAGTCCTGCGAATGAGGGCAGAGTAGATGCAGGCCAAC 229

Db 2271 TCCTCGTAAAGGTCACTCATTCGTCGAGATGAGGGCAGAGTAGATGCAGGCCAAC 2330

Query 230 TGGGAGACGGCCATAGCGGGGAGGTGGGGCTGGGGCTGCCAGCGGGTCTTA 289

Db 2331 TTGGAGACGGCCATGGCACGGGGAGTGTAGGGCAGGGCGTGGGGTCTTA 2390

Query 290 CTACCCGGATGAAGTGGGGCTCACCCAAACGCGCCTTAGCTTCTCGAAGGACCGA 349

Db 2391 GTGGCAGGATGAAGTGGGGCTTACCCCAAACGCGCCTTAGCTTCTCGAAGGACCGA 2450

Query 350 ACACCTTGGGGAGCCGAGGAAGGGGT 378

Db 2451 GCAGCTTGGGGAGCTGAGGAAGGGGT 2479

RESULT 15

US-09-949-016-15546

; Sequence 15546, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. CRAIG ET AL.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15546

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Db 86 GTGGCAGGATGAAGTGGGGCTCACCCAAACGCGCCTTAGCTTCTCGAAGGACCGA 27

Query 350 ACACCTTGGGGAGCCGAGGAAGGGGT 378

Db 26 GCACCTTGGGGAGCTGAGGAAGGGGT 1

1 RESULT 14

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 ORGANISM: Human  
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 NAME/KEY: misc\_feature  
 LOCATION: (1)..(187595)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-949-016-15546

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 Best Local Similarity 85.3%; Pred. No. 1e-66;  
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Search completed: August 20, 2006, 07:17:13  
 Job time : 304 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:46:58 ; Search time 8455 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb\_ph:  
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5: gb\_pr:  
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7: gb\_stB:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vl:  
11: gb\_ov:  
12: gb\_in:  
13: gb\_tm:  
14: gb\_om:  
15: gb\_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						ALIGNMENTS						
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c 6	1431	100.0	156121	5	DQ190452	Homo sapi						
c 7	1431	100.0	156879	5	DQ190453	Homo sapi						
c 8	1431	100.0	161765	5	DQ190451	Homo sapi						
c 9	1431	100.0	167910	5	DQ190450	Homo sapi						
c 10	1429.4	99.9	110669	5	AC060780	Homo sapi						
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c 12	1301.8	91.0	1706	5	AY581858	AY581858 Hylobates						
c 13	1165.6	81.5	1688	5	AY581860	AY581860 Pario anu						
c 14	909.4	63.5	1237	2	AR184045	AR184045 Sequence						
c 15	727.6	50.8	1339	5	AY581855	AY581855 Pan trogl						
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AY589041 Macaca mu  
AY581862 Aotus tri  
CQ787189 Sequence  
CQ806564 Sequence  
AX795672 Sequence  
C0776448 Sequence  
L78833 Homo sapien  
AC135721 Homo sapi  
AR380342 Sequence  
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AY581859 Papio anu  
AY581861 Saginus  
AY273801 Homo sapi  
AC175025 Rhinoloph  
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AC174860 Sub scrof  
AC138235 Homo sapi  
AF227189 Homo sapi  
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AC172475 Bos tauru  
AC168285 Bos tauru  
AC174864 Dasypus n  
AC174852 Oryctolag  
AC175004 Oryctolag  
AX344396 Sequence

ORIGIN

Query Match, Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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**RESULT 4**

DQ190456/c

LOCUS DQ190456

DEFINITION Homo sapiens clone mck578 U neighbor of BRCA1 gene, partial cds; and hypothetical protein LOC10230 (NBR2) and breast cancer 1 early onset (BRCA1) genes, complete cds.

ACCESSION DQ190456

VERSION DQ190456.1 GI:75875068

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 150669)

AUTHORS Raymond, C.K., Paddock, M., Subramanian, S., Deodato, C., Zhou, Y., Haugen, E., Kaul, R. and Olson, M.V.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA

FEATURES source

1. .150669

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ORIGIN

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## ORIGIN

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## RESULT 6

DQ190452/C  
LOCUS DQ190452

DEFINITION Homo sapiens clone mck94 A neighbor of BRCA1 gene 1 (NBR1) gene, partial cds; and hypothetical protein LOC10230 (NBR2) and breast cancer 1 early onset (BRCA1) genes, complete cds.

ACCESSION DQ190452  
VERSION DQ190452.1  
KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Cataarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 156121)  
Raymond, C.K., Paddock, M., Subramanian, S., Decadato, C., Zhou, Y., Haugen, E., Kaul, R. and Olson, M.V.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA

FEATURES Location/Qualifiers

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ORIGIN

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ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 156879)  
AUTHORS Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y., Haugen,E., Kaul,R. and Olson,M.V.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA  
FEATURES Location/Qualifiers

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Raymond, C.K., Paddock, M., Subramanian, S., Deodato, C., Zhou, Y.,  
Haugen, E., Kaul, R. and Olson, M.V.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-2005) Genome Center, Department of Medicine,  
University of Washington, Box 352145, Seattle, WA 98195, USA  
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Qy	541	CCTCGTGACATAAAGAAAGAGACGGAAAGGAATTCTACCTGAGTTGCCGTAA 600	1 (bases 1 to 167910)
Db	23261	CCTGGTGACATAAAGAAAGAGACGGAAAGGAATTCTACCTGAGTTGCCGTAA 23202	Raymond, C.K., Paddock, M., Subramanian, S., Deodato, C., Zhou, Y., Haugen, E., Kaul, R. and Olson, M.V.
Qy	601	GCGCCCGGCCTCTCGCTCTACGCTTCCAGTGCGCTTATTACGTCAAGTAATGCTG 660	Direct Submission
Db	23201	GCGCCCGGCCTCTCGCTCTACGCTTCCAGTGCGCTTATTACGTCAAGTAATGCTG 23142	Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA
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LOCUS	Homo sapiens chromosome 17, clone RP11-242D8, complete sequence.		
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ACCESSION	AC060780		
VERSION	AC060780.18	GI:29126449	HTG.
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		
REFERENCE			
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.		
TITLE	Homo sapiens chromosome 17, clone RP11-242D8		
JOURNAL	Unpublished		
REFERENCE			
AUTHORS	1 (bases 1 to 110669)		
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, P., Boguslavkiy, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McCowan, P., McGurk, A., McKernan, K., McPheeeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M.			
TITLE	Direct Submission		
JOURNAL	Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE			
AUTHORS	3 (bases 1 to 110669)		
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gordyn, S., Horton, L., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keils, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Major, J., Matthews, C., Mihova, V., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.			
TITLE	Direct Submission		
JOURNAL	Submitted (20-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Mar 20, 2003 this sequence version replaced gi:24496797. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a>		
FEATURES			
source	Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: <a href="http://www-seq.wi.mit.edu">http://www-seq.wi.mit.edu</a> Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L7945 Center clone name: 242_D_8		

Only the first 110.7 kilobases of this clone are being submitted. The remainder overlaps accession number AC109326 [WIGGR project L24004].

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repeat_region	complement(2866. .2969)		
repeat_region	3460. .3762		
repeat_region	/rpt_family="AluSx"		
repeat_region	complement(3975. .4101)		
repeat_region	/rpt_family="AluSp/q"		
repeat_region	4157. .4459		
repeat_region	/rpt_family="AluJb"		
repeat_region	4623. .4704		
repeat_region	/rpt_family="MIR"		
repeat_region	complement(4802. .5078)		
repeat_region	/rpt_family="AluSx"		
repeat_region	5148. .5187		
repeat_region	/rpt_family="(TG)n"		
repeat_region	complement(5209. .5258)		
repeat_region	9729. .1040		
repeat_region	/rpt_family="AluJb"		
repeat_region	10525. .10835		
repeat_region	/rpt_family="AluSx"		
repeat_region	10850. .11019		
repeat_region	/rpt_family="AluSc"		
repeat_region	11320. .11389		
repeat_region	/rpt_family="MIR3"		
repeat_region	11398. .11584		
repeat_region	/rpt_family="L12"		
repeat_region	11901. .12031		
repeat_region	/rpt_family="AluSg/x"		
repeat_region	12044. .12275		
repeat_region	/rpt_family="MIR"		
repeat_region	complement(12460. .12745)		
repeat_region	/rpt_family="AluJo"		
repeat_region	12767. .12798		
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repeat_region	complement(12799. .13094)		
repeat_region	/rpt_family="Alusx"		
repeat_region	13095. .13118		
repeat_region	/rpt_family="AT rich"		
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repeat_region	/rpt_family="FLAM_C"		
repeat_region	complement(13249. .13551)		
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repeat_region	complement(13690. .14000)		
repeat_region	/rpt_family="AluSp"		
repeat_region	14479. .14602		
repeat_region	/rpt_family="FLAM_C"		
repeat_region	complement(14769. .14945)		
repeat_region	/rpt_family="AluSg/x"		
repeat_region	14955. .15198		
repeat_region	/rpt_family="(TA)n"		
repeat_region	complement(15235. .15526)		
Query Match	99.9%	Score 1429.4; DB 5; Length 110669;	
Best Local Similarity	99.9%	Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;	
Matches	1430;	Conservative 0; MisMatched 1430;	
Qy	1	CCGTCAGTCAGGCTCTAGGAGCTCAGCGAGCTCAGCGAGTCACGTTTCCCCCTCTAC	60
Db	84323	CCGTCAGTCAGGCTCTAGGAGCTCAGCGAGTCACGTTTCCCCCTCTAC	84382
Qy	61	ATTCAGATGTTGGCTCCATGTTGAGCTTGGGAGCTTGCAACAAAGCCAGGCCA	120
Db	84383	ACTGAGATGTTGGCTCCATGTTGAGCTTGGGAGCTTGCAACAAAGCCAGGCCA	84442
Qy	121	AAAAGTTCAATAATTACACTGGCTGCTTAATAAGGCATTTGATCTTACCTCCGTA	180
Db	85343	GGGCTTATAATGTCACAGTAATGGATTCGGAGTTGGTTATGTTCTCTATCTTGAGAG	85342
Qy	1021	CAGAGACTAGGCCAAAAAGATACCTACAACCTCTAGGAAGACTACGATCCCATCAG	1080
Db	85343	CAGAGACTAGGCCAAAAAGATACCTACAACCTCTAGGAAGACTACGATCCCATCAG	85402
Qy	1081	CCCCACGAGTCGGGCAAGTAGTCCTCTAAGGTCACTGGCCACATCTGGCACTCTAGTC	1140
Db	85403	CCCCACGAGTCGGGCAAGTAGTCCTCTAAGGTCACTGGCCACATCTGGCACTCTAGTC	85462
Qy	1141	GCCGAATTGCTGGGAAGGGAATCCGCTCTGGCCACATCTGGCACTCTAGTC	1200
Db	85463	GCCGAATTGCTGGGAAGGGAATCCGCTCTGGCCACATCTGGCACTCTAGTC	85522
Qy	1201	CGCCCTCAGCCTCATGTTGTTATGTTGTCGGGTCAGGTTGCTCTGGCC	1260
Db	85523	CGCCCTCAGCCTCATGTTGTTATGTTGTCGGGTCAGGTTGCTCTGGCC	85582

Qy	1261 CATCGACGCCAATCTCCACCAATCAATTGGCGTGGTGGTTGAGGGACAAGTGGTGAGGC 1320	Db	303 GCCAAAAGTTCAATATTACACTGGCTGCTTATAAGGCATTCATCTTACCTCCG 362
Db	85583 CATGACGCCAATCTCCACCAATCAATTGGCGTGGTGGTTGAGGGACAAGTGGTGAGGC 85642	Qy	177 TAAAGGTACCTCATAGTCCTCAGAATGAGGGCAGAGTAGTCAGGCAAGCTGGAGA 236
Qy	1321 CAATCATCTGGGAACACTCGGAGAACAGGGGACTAGTTACTGTCTTATCCGCATG 1380	Db	363 TGAAGTCACCTCATAGTCCTGCARAATGAGGGCAGAGTAGTCAGGCAAGCTGGAGA 422
Db	85643 CAATCATCTGGGAACACTCGGAGAACAGGGGACTAGTTACTGTCTTATCCGCATG 85702	Qy	237 CGGAGGCCATAGCGGGGGAGTGAGGTGGGCTGGGCTGCGGAGCGGGTCTACTACCG 296
Qy	1381 TTAGATTCCCCACAGGGATAGGGCAGAGGCCGTAGGGACCTCTG 1431	Db	423 CGGAGGCCATAGGGGGGGAGGTGGGCTGGGCTGCCGAGCGGGTCTACTACCG 482
Db	85703 TTAGATTCCCCACAGGGATAGGGCAGAGGCCGTAGGGACCTCTG 85753	Qy	297 GATGAGTGAGGTCTCACCCACAGGGCTAGCTCTGGAGAGGACACCT 356
		Db	483 GATGAGTGAGGTCTCACCCACAGGGCTAGGGACCTCTG 542
		Qy	357 GGCGGAGGCCAGGGAAAGGGTCCACAGTTTAATTATCTGTAATTCCCACGCTTAC 416
		Db	543 GCGGGAGGCCAGGGAAAGGGTCCACAGTTTAATTATCTGTAATTCCCACGCTTAC 602
		Qy	417 TGTGGCCACGGAAACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACAGTCAG 476
		Db	603 TGTGGCCACGGAAACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACATAGTCAG 662
		Qy	477 AGCAAGGGGGACAGAAAGAGCTAGCATCTCGGGCTCTGGGTTGCCACCCAGTC 536
		Db	663 AGGAAGGGGGACAGAAAGAGCTAGCATCTCGGGCTCTGGGTTGCCACCCAGTC 722
		Qy	537 CTCCCCGGTACATAAAGAAAGAGCTACCTGGT 596
		Db	723 CTCCCCGGTACATAAAGAAAGAGCTACCTGGT 782
		Qy	597 TAAAGGCCGCCCTCTCGCCTCTACGGTCCAGTGAGGCTTACGTACAGTAATT 656
		Db	783 TAAAGGCCGCCCTCTCGCCTCTACGGTCCAGTGAGGCTTACGTACAGTAATT 842
		Qy	657 GCTGTACCAAGGTCAAATGCCACCTTGAGGCTTAATGGGGTCTCCAGT 776
		Db	843 GCTGTACCAAGGTCAAATGCCACCTTGAGGCTTAATGGGGTCTCCAGT 902
		Qy	717 AGCAGCTTAAGAAGAGGTCCATTACCCACTCTTCCGCCATAATGGGGTCTCCAGT 776
		Db	903 AGCAGCTTAAGAAGAGGTCCATTACCCACTCTTCCGCCATAATGGGGTCTCCAGT 962
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		Qy	219. .565
		Db	/rpt_family="ARPP1"
		Qy	/product="BRCA1"
		Db	/number=1
		Qy	/pseudo
		Db	/complement
		Qy	(708. .711)
		Db	817. .1298
		Qy	/note="similar to Homo sapiens NBRI testis isoform exon 1"
		Db	1507. .1510
		Qy	1542. .1657
		Db	/note="similar to Homo sapiens NBRI general isoform exon 1"
		Qy	ORIGIN
		Db	
		Qy	Query Match
		Db	Best Local Similarity 98.0%; Pred. No. 0; Length 1703;
		Qy	Matches 1407; Conservative 2; Mismatches 22; Indels 4; Gaps 1;
		Db	1 CCGTCCAGAACGCTCTAGGGAGCTCACGAGCTCACGACGGGAGTCAGGTTTTTCCCCCT 56
		Qy	183 CGGTCCAGAACGCTCTAGGGAGCTCACGAGCTCACGACGGGAGTCAGGTTTTTCCCCCT 242
		Db	57 CTACATGGAGATGGCTCCAAATGGTGAAGCTGGCAGGACCTTGCAAAACAGCCAG 116
		Qy	243 CTACATGGAGATGGCTCCAAATGGTGAAGCTGGCAGGACCTTGCAAAACAGCCAG 302
		Db	117 GCCAAAAGTTCAATATTACACTGGCTTAAAGGCATTGCTTACCTCCG 176
		Qy	
		Db	1383 GTCGGCCCTCAGCCTCAATGTTGTTGCTTCGGGTCAGGTGCTCTGCC 1442

RESULT 12

AY581858 AY581858 1706 bp DNA linear PRI 13-NOV-2004

DEFINITION Hylobates lar NBR1 testis isoform-like and NBR1 general isoform-like genes, complete sequence.

ACCESSION AY581858

VERSION AY581858.1 GI:51104370

KEYWORDS

SOURCE

ORGANISM Hylobates lar (common gibbon)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hylobatidae; Hylobates.

REFERENCE 1 (bases 1 to 1706)

JOURNAL Roberts,R.G., Selfe,J., Jin,H., Whitehouse,C. and Solomon,E. and Roberts,R.G.

STRUCTURAL evolution of the BRCA1 genomic region in primates

AUTHORS 2 (bases 1 to 1706)

JOURNAL Genomics 84 (6), 1071-1082 (2004)

TITLE Direct Submission

JOURNAL Submitted (18-MAR-2004) Division of Medical and Molecular Genetics, GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London SE1 9RT, UK

FEATURES source

1. 1706 Location/Qualifiers

/organism="Hylobates lar"

/mol-type="genomic DNA"

/db\_xref="taxon:9580"

218. .565 /rpt\_family="ARPP1"

/complement(501. .670)

/product="BRCA1"

/pseudo /number=1

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CAAT\_signal

misc\_feature

CAAT\_signal

misc\_feature

exon

complement (708. .711)

817. .1301 /note="similar to Homo sapiens NBR1 testis isoform exon 1"

1510. .1513 1545. .1660 /note="similar to Homo sapiens NBR1 general isoform exon 1"

ORIGIN

Query Match 91.0%; Score 1301.8; DB 5; Length 1706;

Best Local Similarity 95.5%; Pred. No. 0; Mismatches 57; Indels 8; Gaps 3; Matches 1374; Conservative 0;

QY 1 CCGTCCAGAAGCTCTCAGGGAGCTCACGCCGCGAGTCACCCRTT---TTTCCCCCT 56

Db 182 CCGTCCAGAAGCTCTCAGGGAGCTCACGCCGCGAGTCACCCRTTTCCTCCC 241

QY 57 CTACATTGCAAGTGTGGCTCCAATGTGTGGCCAGGACCTTGCAAAACAGCAG 116

Db 242 CTACATTGCAAGTGTGGCTCCAATGTGTGGCCAGGACCTTGCAAAACAGCAG 301

QY 117 GCCAAAAGTTCAATATTACACTGGCTGCTTAATAAGGCATTGACTTACCTCCG 176

Db 1563 CATGTTAGATTCAACCCCCAACAGGGATAGGGCAGACCGGGTAGGGCTCTTG 1617

QY 1257 GCCCCATGGCAATCTCCACCAATCAATGGGGTGTGTTGAGGACAAGTGGTGA 1316

Db 1443 GCCCATGGCAATCTCCACCAATCAATGGGGTGTGTTGAGGACAAGTGGTAA 1502

QY 1317 GAGCCAATCATCTGGGAGAACAGGGGACTAGTTACTGTCTTATCCGC 1376

Db 1503 GAGCCAATCATCTGGGAGAACAGGGAGACTAGTTACTGTCTTATCCGC 1562

QY 1377 CATGTTAGATTCAACCCCCAACAGGGATAGGGCAGACCGGGTAGGGCTCTTG 1431

Db 1563 CATGTTAGATTCAACCCCCAACAGGGATAGGGCAGACCGGGTAGGGCTCTTG 1617

QY 357 GGCGCGAGCCGAGGAA-GGGTTCCACCTTAATTATCTGAATTCCACGCTTA 415

Db 542 GGCGCGAGCCGAGGAAAGGGGTCCACAGTTATTCTGTAATTCCACGCTTA 601

416 CTGTCGCCACGGAAACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACAGTC 475

Db 602 CTGTTCCACGGAAACCGCTGAGCAATAGCCTCTCAGAATAGGAATCAAGACACAGTC 661

QY 476 GAGGAAGGGGGACAGAAAGACCTAGCATCTCTGGGCTCTGGGTGGCCACCCAGT 535

Db 662 GAGGAAGGGGGACAGAAAGACGGCTAGGTCTCTGGGTCTCTGGATGGCCACCCAGT 721

536 CCTCCCTGGTGCATAAAAGAAAGAGACGGAAAGGAAGATTCTACCTGAGTTGCC 595

Db 722 CCTCCCTGGTGCATAAAAGAAAGAGACGGAAAGGAAGATTCTACCTGAGTTGCC 781

QY 596 GTAAAGCCCCCCTCTGCCCTACGCTCCAGTGCGGTTTACGTACAGTAAT 655

Db 782 ATAAGGCCCGCCCTTGGCTCTACGCTCCAGTGCGGTTTACGTACAGTAAT 841

QY 656 TGCTGACCAAGGTCAAGAATGCCACCTGAGGTCCATTACCCACTCTTCGCC 715

Db 842 TGCTGACCAAGGTCAAGAATGCCACCTGAGGTCCATTACCCACTCTTCGCC 901

QY 716 AAGCAGTCTAAGAAGAGGTCCATTACCCACTCTTCGCC 775

Db 902 AAGCAGTCTAAGAAGAGGTCCATTACCCACTCTTCGCC 961

QY 776 TTAGGTAAATAAAGGATTGTGGAGGGAAAGAACTACTATTCCACATGC 835

Db 962 TTAGGTAAATAAAGGATTGTGGAGGGAAAGAACTACTATTCCACATGC 1021

QY 836 A---TTGGGAAGGAAAGGCCTGGCCAACGTGTTCTGGAAACTTGCAG 892

Db 1022 ATTTGGGGAAACGAAGGGCTTGGCCAACGTGTTCTGGAAACTTGCAG 1081

QY 893 AGGAACATCCAATCCAAGGGCACAACTCTCAGGAATTCACAGTAGATTGAG 952

Db 1082 AGGAACATCCAATCCAAGGGCACAACTCTCAGGAATTCACAGTAGATTGAG 1141

QY 953 ACCTCCGGGCTTACATGTCAACAGTAATGGATTGGAGTTGTATGTTCTCTAT 1012

Db 1142 ACCTCCGGGCTTACATGTCAACAGTAATGGATTGGAGTTGTATGTTCTCTAT 1201

QY 1013 CTTGAGAGCAGACTAGGGAAAAAGATACTACAACCTCTAGGAAGACTACGATC 1072

Db 1202 CTTGAGAGCAGACTAGGGAAAAAGATACTACAACCTCTAGGAAGACTACGATC 1261

QY 1073 CCATCCAGCCCCACGGAGCTCGGCCAAGTAGTCCTCAAGGTCACTGGCTGGGGAGC 1132

Db 1262 CCATCCAGCCCCACGGAGCTCGGCCAAGTAGTCCTCAAGGTCACTGGCTGGGGAGC 1321

QY 1133 CAGTGGGGCGAATTGGCTGGGAAGGGAAATCCGCTCTGGCCACATCTGCCACT 1192

Db 1322 CAGTGGGGCGAATTGGCTGGGAAGGGAAAGCCGCTCTGGCCACATCTGCCACT 1381

QY 1193 CCTAGTCCAGCCCCACGGAGCTCGGCCAAGTAGTCCTCAAGGTCACTGGCTGG 1252

Db 1382 GGTAGTCCGCCCCACGGAGCTCGGCCAAGTAGTCCTCAAGGTCACTGGCTGG 1441

RESULT 13

QY 1 253 CCCGCCCATCGACGCAATCTCCACCAATCATTGGCTGGTTGAGGAGACTG 1312  
LOCUS AY581860 1688 bp DNA linear PRI 13-NOV-2004  
DEFINITION Papio anubis BRCA1 pseudogene, NBRI testis isoform-like, and NBRI  
General isoform-like Genes, complete sequence.

ACCESSION AY581860  
VERSION AY581860.1 GI:51104372  
KEYWORDS  
SOURCE  
ORGANISM Papio anubis (olive baboon)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Cercopithecidae; Cercopithecinae; Papio.

REFERENCE  
AUTHORS Jin,H., Selfe,J., Whitehouse,C., Morris,J.R., Solomon,E. and  
Robert,R.G.  
TITLE Structural evolution of the BRCA1 genomic region in primates  
JOURNAL Genomics 84 (6), 1071-1082 (2004)  
PUBMED 15533724  
2 (bases 1 to 1688)

ROBERTS, R.G., SELFE, J., JIN, H., WHITEHOUSE, C. and SOLOMON, E.  
DIRECT SUBMISSION  
Submitted (18-MAR-2004) Division of Medical and Molecular Genetics,  
GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London  
SE1 9RT, UK  
LOCATION/QUALIFIERS  
1. Location/Qualifiers  
source  
1. 1688

FEATURES  
source  
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complement  
product="BRCA1"  
number=1  
pseudo  
complement (695. .698)  
804. .1283  
/note="similar to Homo sapiens NBRI testis isoform exon 1"  
1492. .1495  
1537. .1642  
/note="similar to Homo sapiens NBRI general isoform exon 1"  
ORIGIN

Query Match 81.5%; Score 1165.6; DB 5; Length 1688;  
Best Local Similarity 91.2%; Pred. No. 0; Mismatches 114; Indels 12; Gaps 6;  
Matches 1306; Conservative 0; MisMatches 114; Indels 12; Gaps 6;

QY 1 CGGTCCAGAACGCTCTAGGGAGCTCAGGAGCTCACGTTTTCCTCCCTCTAC 60  
Db 182 CGGTCCAGAACGCTCTAGGGAGCTCAGGAGCTCACGTTTTCCTCCCTCTAC 60  
61 ATGCAGATGTCCTCCAATGTTGAGCTTGCAACAAAGCCAGGCC 120  
Db 239 ATGCAGATGAGGCTCCAGTGTGACGTTGGCCAGGGCTTGCACACAGCCAGGCC 298  
QY 121 AAAGTTCAATTACACTGGCTCTTAATAAGGCATGTATCTCCCGTAA 180

Db 299 AAAATGTTCAACATTACACCGGCTCTTAATGAGGCATTGATCTACTCTCCGTGAC 358  
QY 181 GGTCA CCTCATAGTCCTGCGAATGAGGGCAGAGTAGTCAGGCAAGCTGGAGACGGA 240  
Db 359 GCTCACCTCATCGTCGGGCAGAATGAAGGCAGAGTAGTCAGGCAAGCTGGAGACGTA 418  
QY 241 GGCATAGCGCGGGAGTGTGGGCTGGGCTGGGGAGCGGGTACTCACCGGATG 300  
Db 419 GGCCATGGCGGGAGTGTGGGCTGGGGAGCGGGTACTGCCAGAGGGGTCTAGTGCAGGAG 478  
QY 1373 CGGCCATGTTAGATTCACCCACAGGGATAGGGCAGAGCCGGTAGGGCTCTTG 1431  
Db 1562 CGGCCATGTTAGATTCACCCACAGGGATAGGGCAGAGCTGGCGAGCGACCTGGG 1620

Db QY 361 GCAGCGGAGGAAAGGGGTCACAGTTAATCTGTAAATCCCACCGTTACTGT 420  
Db 539 GCAG-CGAGGAAGGGTCCACAGTTAATCTGTAAATCCCACCGTTACCGTT 597  
QY 421 GCCACGGAAACCGCTGAGCAATAGCCTCTCGAAATAGGAATCAAGACACAGTCAGGAA 480  
Db 598 GCCACGGAAACCGCTGAGCAACAGCCTCTCGAAATAGGAATCAAGACA---CAGAGGA 653  
QY 481 AGGGCGGACAGAAAGAGCCTAGCATCTCGGGCTCTGGTTGGCCACCCAGTCCTCC 540  
Db 654 AGGGAGGGACAGAAAGAGCCTATCGTCTCGGGCTCTGGATTGGCCACCCAGTCCTCC 713  
QY 541 CCTGGTACATAAAAGAAAGAGACGGAAAGGAATTCTACCTGAGTCAGGTCGGCGTAA 600  
Db 714 CGGGGTGACGTAAGAAAGAGACGGAAAGGAATTCTACCTGAGTCAGGTCGGCGTAA 773  
QY 774 GCGCCCGCCCTCTCGCTT"AGCTTCAAGT"GCAGTTAGCTTACAGTCAAGTA 833  
Db 601 TACCAAGGTAGAATGCCACTTGAGCTGAATATCAGCTAAGTTCAGTAATGCTG 660  
QY 834 TACAAGATCAGAATCGCTACCCGAGGCTGATAATGAGTGTAGTCCAAAGCA 893  
Db 721 GTCTTAGAGAGGGTCCATTACCCACTCTTCCGCTTAATGGAGTAGTGTCAAAGCA 720  
QY 894 GTCGTAGGAAGAGTCCCATCCCTACTCTTCCGCTTAATGGAGGTCTCCAGTTAG 780  
Db 953  
QY 781 GTAATAAAGGATGTTGGAGGGAAAGAACTACTATTCACATGCATTC 840  
Db 954 GTAATAAAGGATGTTGGGGGTGGAGGGAAAGAACTACTATTCACATGCATTC 1013  
QY 841 GGAACGAAAGGCTGGCCACACTGTCCTGGAAACTGTAGTCTATGGAGAGGACAT 900  
Db 1014 GGAATTAAGGATGTTGGGGGTGGAGGGAAAGAACTACTATTCACATGCATTC 1073  
QY 901 CCAATACCAAAAGGGACAATTCTCAGGAATCCAGTGGATAGTGGAGACCTCC 960  
Db 1074 CCAATACCGAAGGGGACAATTCTCAGGAATCCAGGGATAGTGGAGACCTCC 1133  
QY 961 GGGCTTATACATGTCACAGTAATGGATGGAGTGTATGTTCTCTATCTGAGAG 1020  
Db 1134 GCGCTTATACATGTCACAGTGGACTGGAGTGTGT 1193  
QY 1021 CAGAGACTAGGCCAAAAGATACTACAACCTCTAGGAAGACTACGATCCCATCCAG 1080  
Db 1194 CAGAGACTAGGCC- AAAAGATACCGACAACCTCTAGGAAGACTACATCCATCCAG 1251  
QY 1081 CCCACAGAGTCTGGGAAGGGAAATCCGCTCTGCCACATCTGCCACTCTAGT 1139  
Db 1252 CCCACAGAGTCTGGCAAGTGTCTCTAAGGTCACTGGCCTGC- GGGACGCCAGTGC 1311  
QY 1140 CGCCGAATTGCTGGCAAGTGTCTCTAAGGTCACTGGCCTGC- GGGACGCCAGTGC 1199  
Db 1312 CGCCGAATTGCT- AGGAAGGGAAATCCGCTCTGCCACGCTCTCCACTCTGAGT 1370  
QY 1200 CGGCCCTCAGCCTCAATGTTGTTATGTTGTCAGGTTCTGCCCCGG 1259  
Db 1371 CGCCGAATTGCT- AGGAAGGGAAATCCGCTCTGCCACGCTCTCCACTCTGAGT 1430

RESULT 14

QY 1260 CCATCGACGCCAATCTCCACCAACTCAATGGCGTGTGTTGGAGGAACAGTGGTAGAG 1319  
Db 1431 CCGTGCAGAGAACTCCACCAACTCAATGGGTGTGTTGGAGAACGGTAGAG 1490

QY 1320 CCAAATCATCTGGGAACACTCGGAGAACAGGGACTAGTACTGTCTTATCCGCAT 1379  
Db 1491 CCAAATCATCTGGGAACACTCGGAGAACAGGGACTAGTACTGTCTTATCCGCAT 1550

QY 1380 GTTAGATTACCCACAGGATAGGGGGAGGCCAGGGTAGGGGACGGTCTTG 1431  
Db 1551 GTTAGATTACCCACAGGATAGGGGGAGGCCAGGGTAGGTGGCAGGGACTGTCTTG 1602

REFERENCE AR184045  
AUTHORS Holt, J.T., Jensen, R.A., Page, D.L., Obermiller, P.S.,  
ACCESSION AR184045  
TITLE Method for detection and treatment of breast cancer  
VERSION 1.0  
JOURNAL Patent: US 6342483-A 48 29-JAN-2002;  
FEATURES Location/Qualifiers  
SOURCE 1. .1237  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 63.5%; Score 909.4; DB 2; Length 1237;  
Best Local Similarity 94.0%; Pred. No. 5.7e-258;  
Matches 999; Conservative 0; Mismatches 36; Indels 28; Gaps 4;

QY 381 CACAGTTTAATTATCTGTAATCCACGCTTACTGTGCCACGGAA----- 429  
Db 131 CGCAGTTTAATTATCTGTAATCCACGGCTTTCGGTCCACGGAAACGGGCT 190

QY 430 ACCGGCTGAGCAATAGCCTCTAGAATAGGAATCAAGACACAGTCAGGGAAGGGGG 489  
Db 191 ACCGCTAAGCAGCAGCCTCTAGAATACGAATACGGTACAATCAGGGAAGGGGA 250

QY 490 CAGAAAGAGCTAGCATCTCGGGGCTCTGGGTGGCCACCCAGTCCCTCCCTG-TGA 548  
Db 251 CAGAAAGAGCCAAGGGCTCTGGATGGCCACCCAGTCTGCCCCGGATGA 310

QY 549 CATAAAAGAAGAGACGGAAAGGAATCTACCTGAGTCGGCTAAAGCCCCGC 608  
Db 311 CGTAAGGAAAGAGACGGAAAGGAATCTACCTGAGTCGGCTAAAGCCCCGC 370

QY 609 CCTCTCGCTCTACGCTTCAGTTACGTACAGTCGGCTAAAGCCCCGC 668  
Db 371 CCTCTCGCTCTACGCTTCAGTTACGTACAGTCGGCTAAAGCCCCGC 430

QY 669 TCAGAAATGCCACCTGAGGCTGAATATCGCTAAGATAGTCGAAGCAGTCTTAAG 728  
Db 431 TCAGAAATGCCACCTGAGGCTGAATATCGCTAAGATAGTCGAAGCAGTCTTAAG 490

QY 729 AAGGGTCCATTACCCACTCTTCGCCATAATGGAGGTCCAGTTAGGAAATAA 788  
Db 491 AAGGGTCCATTACCCACTCTTCGCCATAATGGAGTCCTCCAGTTAGGAAATAA 550

QY 789 AAGGGTGTGGAGGGAGAACTACTATTCACATGCATGGGGACGAA 848  
Db 551 AAGGGTGTGGAGGGAGAACTACTATTCACATGCATGGGGACGAA 610

QY 849 AGGCCTGCCACACTGTCTGGAAACTGTAGTCTATGGAGGAGAACATCCAAATACC 908

REFERENCE AR184045  
AUTHORS Holt, J.T., Jensen, R.A., Page, D.L., Obermiller, P.S.,  
ACCESSION AR184045  
TITLE Method for detection and treatment of breast cancer  
VERSION 1.0  
JOURNAL Patent: US 6342483-A 48 29-JAN-2002;  
FEATURES Location/Qualifiers  
SOURCE 1. (bases 1 to 1237)

ORIGIN

Query Match 63.5%; Score 909.4; DB 2; Length 1237;  
Best Local Similarity 94.0%; Pred. No. 5.7e-258;  
Matches 999; Conservative 0; Mismatches 36; Indels 28; Gaps 4;

QY 835 GTCCTGGGCAAGTAGTCTCTAAGGTCAAGTGGCTCGGGGACGGAGGGCGAATT 894  
Db 895 TGCCTGGGAAAGGGAAATCCCTCTGGCCACATCTGCGCACTCCTAGTCCGCCCTC 1208

QY 1149 AGCCTCAATGTTGTATGTGTTGTCGGTCAAGGTGCTCTGCCGCCATCGACG 1268  
Db 955 AGCATCAAATGTTGTATGTGTTGTCGGTCAAGGTGCTCTGCCGCCATCGACG 1014

QY 1269 CAATCTCCACCAATCAATGGCGCTGTCGTTGAGGACAAGTGGTAGGCCATATC 1328  
Db 1015 CAATCTCCACCAATCAATGGCGTGGTTGAGGACAAGTGGTAGGCCATATC 1074

QY 1329 TTGGGAAACTCGGAGAACAGGGACTAGTTACTGTCTTATCCGCCATGTTAGATTC 1388  
Db 1075 TTGGGAAACTCGGAGAACAGGGACTAGTTACTGTCTTATCCGCCATGTTAGATTC 1134

QY 1389 ACCCCACAGGATAGGGCAGAGCCGGTAGGGGACGGTCTTG 1431  
Db 1135 ACCCCACAGGATAGGGCAGAGCCGGTAGGGGACGGTCTTG 1177

RESULT 15

QY 1581855 AY581855 1339 bp DNA linear PRI 13-NOV-2004

REFERENCE AY581855  
AUTHORS Jin, H., Selfe, J., Whitehouse, C., Morris, J.R., Solomon, E. and  
ACCESSION AY581855  
TITLE Structural evolution of the BRCA1 genomic region in primates  
VERSION AY581855.1 GI:51104367  
FEATURES Pan troglodytes (chimpanzee)  
SOURCE Pan troglodytes  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1339)  
AUTHORS Jin, H., Selfe, J., Whitehouse, C., Morris, J.R., Solomon, E. and  
ACCESSION AY581855  
TITLE Structural evolution of the BRCA1 genomic region in primates  
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REFERENCE 2 (bases 1 to 1339)  
AUTHORS Roberts, R.G., Selfe, J., Jin, H., Whitehouse, C. and Solomon, E.  
TITLE Direct Submission  
JOURNAL Submitted (18-MAR-2004) Division of Medical and Molecular Genetics, GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London SE1 9RT, UK  
FEATURES Location/Qualifiers

1. .1339  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/complement(110. .290)

misc\_feature /note="similar to Homo sapiens BRCA1 exon 1"  
misc\_feature complement(374. .377)  
/note="similar to Homo sapiens NBR2 exon 1"

ORIGIN	CAAT_signal	1154. .1157	Db	1155 AATCTCTGGGAAACGGGAGAAC--GGGACTAGTTACTGTCTTATCCGCCATGT 1212
Query	Match 50.8%; Score 727.6; DB 5; Length 1339;		Qy	1382 TAGATTCACCCACAGGGATAGGGCAGAGCCGGTAGGGACGGCTCTTG 1431
Best Local Similarity 85.8%; Pred. No. 5.2e-204;			Db	1213 TAGATTCACCCACAGAGATAGGGCAGGGAGGGCTCTTG 1262
Matches 918; Conservative 0; Mismatches 104; Indels 48; Gaps 8;				
Db	222 CGCAGTTTAATTATCTGTAATTCCGGCTTTCCGTGCAACGGAAACCGGGCT 281			
Qy	381 CACAGTTTAATTATCTGTAATTCCACGTTACTGTGCCACGGAA----- 429			
Db	282 ACCGCTAAGCAGCAGCCTCTCGAATACGAATCAGGTACATCAGGGATGGAGGA 341			
Qy	430 ACCGCTGAGCAATAGCCTCTCGAATAGGAATCAAGACACAGTCAGGGAGGGGG 489			
Db	342 CAGAAAGAGCAAGCGTCCTCGGGCTCTGGATGGCCACCCAGTCCTCCCTGG-TGA 401			
Qy	490 CAGGAAGAGCTAGCATCTCTGGGGCTCTGGTGGCCAACCGAGTCCTCCCTGG-TGA 548			
Db	549 CATAAAAAGAAGAGACGGAAAGGAAGAACTACCTGAGTCGGCTAAAGCCCCGC 608			
Qy	402 CGTAAAGGAAGAGACGGAAAGAGGAAGGGAGATTCTACCTGAGTCGGCTAAAGTGCCTGC 461			
Db	609 CCTCTCGCCCTCTACGCTCCAGTGTGGCTTATGCATCACAGTAATGCTGTAAGG 668			
Qy	669 TCGAAATGCCAACCTGAGGCCCTGAATATCAGCTAAGATAGTGTCAAAGCAGTCTTAAG 728			
Db	522 CCTCTAGCCTACTCTTCCAGTGTGGCTTATGCATCACAGTAATGCTGTAAG 521			
Qy	729 AAGGGTCCATTACCCACTTTCCGCCTAATGGGGCTTATTACGGTCAAGTTAGGAAATAA 788			
Db	558 AAGGGTCCCAATCCCCCACTCTTCCGCCTAATGGGGCTTATTACGGTCAAGTTAGGAAATAA 617			
Qy	789 AAGGATGTTGGGGTGGAGGAAAG-----AACTACTATTCCAAATGCAATTGGGA 843			
Db	618 AAGGAAATAAGGATGTTGGGGGGGGAGGAATAATTATTTCCAGCATGGTGGGA 677			
Qy	844 ACGGAAGGCCCTGGCCACACTGTTCTTGGAAACTGTAGCTTATGGAGAGGAATCTCA 903			
Db	678 ATGAAAGGTCTTGCACACTGTTCTTAGAAACTGTAGCTTATGGAGAGGAACATCCA 737			
Qy	904 ATACCAAAAGGGCACATTCTCAGGAATTCAGTGGATAGATGGAGACCTCCGGGG 963			
Db	738 ATACCAAGGGGACAATTCTCAGGAATTCAGTGGATAGATGGAGACCTCTGGCGG 797			
Qy	964 CTTATACATGTCAACAGTAATGGATTGGAGTGTGTATGGTCTCTATCTGAGAGCAG 1023			
Db	798 CTGTACTGTCAACAGTTATGGACTGAAACTGTGTATGGTCTCTATCTGAGAGCAG 857			
Qy	1024 AGACTAGGCCAAAAAGATAACCTACAACTC-CTAGGAAGACTACGGATCCCACATCAGCC 1082			
Db	858 AAACTAGGCTTAAAGATAACTACAACCTCTAGGGAGACTACAATTCCATCCAGCC 917			
Qy	1083 CCACGGCTCTGGGCAAGTAGTCCTTAAGGTCACTGGCTCGGGGACGGCAGTGGGGC 1142			
Db	918 CCAGGAGTCCTGGGCAAGTAGTCCTTAAGGTCACTGGCTCGGGGAGTCAGTGGCAGGCC 977			
Qy	1143 CGAATTTCGCTGGGAAGGGAAATCCGCTCGGCCACATCTGGCACTCTAGTTCG 1202			
Db	978 CGAATTTCGCTGGGCAAGGGAAATCCGCTCGGCCATGTCCTGGCACTCTAGTTCG 1037			
Qy	1203 CCCCTCAGCTCAATGTTATTGTTCTGGGTTCAGGTGCTCTGGCCCC-CCCC 1261			
Db	1038 CCTCTCAGCCCCAGTGTGTTTCTGCTTCTGCCCCCTCTCC 1094			
Qy	1262 ATCGACGCCATCTCCACCAATCAATGGCTGGCTGGTGTGAGGGACAAGTGGTGAAGGCC 1321			
Db	1095 GTCGACGCCATCGCCACCGCTCAATGGGTGGTGTGAGGGACAAGTGGTGAAGGCC 1154			
Qy	1322 AATCATCTGGCGAACACTCGGAGAACAGGGACTAGTTACTGTCTTATCCGCCATGT 1381			

Search completed: August 20, 2006, 07:12:06  
Job time : 8459 sec

ID	ACC69622	standard; DNA; 2941 BP.	Qy	301	AAGTGGGGCTCACCCCAACGCCCTTAGCTTCCTCGGAAGGACCGAACCTTGGCG	
XX	AC		Db	1851	AAGTGGGGCTCACCCCAACGCCCTTAGCTTCCTCGGAAGGACCGAACCTTGGCG	
XX	DT	18-JUL-2003 (first entry)	Qy	361	GCAGCGGAAAGGGTTCCAGTTTAATTATCGTAATTCCACGTTACTGTT	
XX	DR	Human tumour-specific promoter nucleotide sequence SEQ ID NO:1.	Db	1911	GCAGCGGAAAGGGTTCCAGTTTAATTATCGTAATTCCACGTTACTGTT	
XX	KW	Human; tumour-specific promoter; tumour; cytostatic; ovarian cancer; gene therapy; ds.	Qy	421	GCCACGGAAACCGCTAGCAATAGCTCTCGGGCTCTGGGTGGCCACCGTCTGGCG	
XX	OS	Homo sapiens.	Db	1971	GCCACGGAAACCGCTAGCAATAGCTCTCGGGCTCTGGGTGGCCACCGTCTGGCG	
XX	PN	WO2003025190-A1.	Qy	481	AGGGGGACAGAAAGAGCTAGCACTCTCGGGCTCTGGGTGGCCACCGTCTGGCG	
XX	PD	27-MAR-2003.	Db	2031	AGGGGGACAGAAAGAGCTAGCACTCTCGGGCTCTGGGTGGCCACCGTCTGGCG	
XX	PP	30-JAN-2002; 2002WO-JP000724.	Qy	541	CCTGGTACCATAAAGAAAGAGCTAGCACTCTCGGGCTCTGGGTGGCCACCGTCTGGCG	
XX	PR	14-SEP-2001; 2001JP-00279088.	Db	2091	CCTGGTACCATAAAGAAAGAGCTAGCACTCTCGGGCTCTGGGTGGCCACCGTCTGGCG	
PA	(PRIM-) PRIMITIVE KK.		Qy	601	GCCCCGGCCTCTCGCTCTACGCTTCCAGTTCGGCTTATTACGTACAGTAATGCTG	
XX	PI	Hamada K;	Db	2151	GCCCCGGCCTCTCGCTCTACGCTTCCAGTTCGGCTTATTACGTACAGTAATGCTG	
DR	WPI; 2003-313358/30.		Qy	661	TACCAAGGTAGATCCACCTGAGGCTGAATATCAGGTAAGATACTGTCAGTTAG	
XX	PT	Tumor-specific promoter for producing e.g. transformant adenovirus to highly proliferate in ovarian cancer cells, applicable in gene therapy for treating ovarian cancer.	Db	2211	TACCAAGGTAGATCCACCTGAGGCTGAATATCAGGTAAGATACTGTCAGTTAG	
XX	PS	Claim 1; Page 34-36; 41pp; Japanese.	Qy	721	GTCTTAAGAAGAGGTCCATACCCACTCTTCGGCCCTTATTACGTACAGTAATGCTG	
CC	The present sequence represents a human tumour-specific promoter (1). The present invention describes the human tumour-specific promoter comprising bases from 1126-2941 or 2501-2941 in the sequence of (1) with 2941 base pairs. Also described: (1) another tumour-specific promoter hybridisable with the specified base sequence under stringent conditions and having a promoter function as such base sequence; (2) a cytotoxic tumour-specific virus with modification to the viral gene by using the tumour-specific promoter to cause specific proliferation in tumour cells or tissue; and (3) treating tumours by administration of such virus to human. (1) has transformant adenovirus to highly proliferate in ovarian cancer cells, which is applicable in gene therapy for treating ovarian cancer. When applied in clinical use, the produced transformant virus has reduced side effects, and therefore larger quantities can be administered	Db	2271	GTCTTAAGAAGAGGTCCATACCCACTCTTCGGCCCTTATTACGTACAGTAATGCTG		
CC	CC	CC	Qy	781	GTAAATAAGGATGTGGAGGTGGAGGAACACTATTCCAACATGCTTCAGTTAG	
CC	CC	CC	Db	2331	GTAAATAAGGATGTGGAGGTGGAGGAACACTATTCCAACATGCTTCAGTTAG	
CC	CC	CC	Qy	841	GGAACGMAAG3CCTGGCCACACTGTCTTGAAACTGTAGTCTATGGAGAGGACAT	
CC	CC	CC	Db	2391	GGAACGMAAG3CCTGGCCACACTGTCTTGAAACTGTAGTCTATGGAGAGGACAT	
CC	CC	CC	Qy	901	CCAAATACCAAGGGGACAATTCTCACGAAATCCAGTGGATAGATGGAGACCTCCG	
CC	CC	CC	Db	2451	CCAAATACCAAGGGGACAATTCTCACGAAATCCAGTGGATAGATGGAGACCTCCG	
CC	CC	CC	Qy	961	GGCTTATACATGTCAACAGTAATGGATGGAGGTGTATGGCTCTATCTGAGAG	
CC	CC	CC	Db	2511	GGCTTATACATGTCAACAGTAATGGATGGAGGTGTATGGCTCTATCTGAGAG	
XX	Sequence 2941 BP; 717 A; 825 C; 690 G; 709 T; 0 U; 0 other;	SQ	Qy	1021	CAGAGACTAGCCAAAAAAGATACTACACCTCTAGGAAAGCTAGATCCATCCAG	
Qy	1	CCGTCAGAACGGCTCAGGGGAGCTCACGACGGCAGTCAGCTTTTCCCCTCTAC	1080	Qy	1081	CCCCACGGAGTCTGGGCAAGTAGTAGTCCTCTAAGGCTCTGGCTCTGGGGAGCGAGTGGC
Db	1551	CCGTCAGAACGGCTCAGGGGAGCTCACGACGGCAGTCAGCTTTTCCCCTCTAC	60	Db	2571	CAGAGACTAGCCAAAAAAGATACTACACCTCTAGGAAAGCTAGATCCATCCAG
Qy	61	ATTCAGATGTGGCTCCAAATGTTGACGGTGGCCAGGACCTTGAACAAAGCCAGGCC	1610	Qy	1081	CCCCACGGAGTCTGGGCAAGTAGTAGTCCTCTAAGGCTCTGGCTCTGGGGAGCGAGTGGC
Db	1611	ATTCAGATGTGGCTCCAAATGTTGACGGTGGCCAGGACCTTGAACAAAGCCAGGCC	120	Db	2631	CCCCACGGAGTCTGGGCAAGTAGTAGTCCTCTAAGGCTCTGGCTCTGGGGAGCGAGTGGC
Qy	121	AAAAGTTCAATATTACACTGGCTGTTAAGGCAATTGATGCTTATCCTCCGTAA	180	Qy	1141	GGCGAATTGGCTGGGAAATCGGCTCTGGCCACATCTGCACTCTAGTC
Db	1671	AAAAGTTCAATATTACACTGGCTGTTAAGGCAATTGATGCTTATCCTCCGTAA	1670	Db	2691	GGCGAATTGGCTGGGAAATCGGCTCTGGCCACATCTGCACTCTAGTC
Qy	181	GGTCACCTCATGGCTGAGATGAGGGAGTAGATGAGGGAAAGCTGGCTCTGGCCACCGT	1730	Qy	1201	GGCGAATTGGCTGGGAAATCGGCTCTGGCCACATCTGCACTCTAGTC
Db	1731	GGTCACCTCATGGCTGAGATGAGGGAGTAGATGAGGGAAAGCTGGCTCTGGCCACCGT	240	Db	2751	GGCGAATTGGCTGGGAAATCGGCTCTGGCCACATCTGCACTCTAGTC
Qy	241	GGCCATAGGGGGAGTGTGGGAGTGGCTGAGGACGGGGGTACTACCGGATG	1790	Qy	1261	CATGGCACTCTCCACCAATCAATGGCTGGCTCTGGCCACATCTGCACTCTAGTC
Db	1791	GGCCATAGGGGGAGTGTGGGAGTGGCTGAGGACGGGGGTACTACCGGATG	1850	Qy	1321	CATGGCACTCTCCACCAATCAATGGCTGGCTCTGGCCACATCTGCACTCTAGTC
Qy	2871	CAATCACTGGGAACTCGGAGAACAGGGAGTAGTACTGTCTTATCCGGCATG	2930	Qy	2871	CAATCACTGGGAACTCGGAGAACAGGGAGTAGTACTGTCTTATCCGGCATG

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Qy 1381 TTAGATTCAAC 1391  
Db 2931 TTAGATTCAAC 2941